

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 17, 2005, 08:52:18 ; Search time 25 Seconds

(Without alignments)
1397.430 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488

Sequence: 1 MFLLATYFPLPLDLMSAE.....PVMLTALALSLVSLAETS 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488	100.0	468	3	US-08-802-805D-21
2	2488	100.0	468	4	US-08-837-199A-4
3	2488	100.0	468	4	US-08-860-370-2
4	2488	100.0	468	4	US-09-187-906-2
5	2488	100.0	468	4	US-08-861-990-1
6	2488	100.0	468	4	US-09-388-316C-21
7	2316.5	93.1	465	4	US-08-837-199A-2
8	2316.5	93.1	465	4	US-09-388-316C-22
9	2311.5	92.9	463	4	US-08-837-199A-12
10	2310.5	92.9	465	4	US-08-861-990-8
11	2309.5	92.8	465	4	US-08-837-199A-6
12	2306.5	92.7	463	4	US-08-837-199A-10
13	2278	91.6	460	3	US-08-802-805D-22
14	2278	91.6	460	4	US-09-187-906-11
15	1686	67.8	346	4	US-09-187-906-9
16	1431.5	57.5	294	4	US-08-837-199A-16
17	1431.5	57.5	294	4	US-08-837-199A-16
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19	1120.5	45.0	464	3	US-08-957-063-6
20	1120.5	45.0	464	3	US-09-487-685-6
21	1120.5	45.0	464	3	US-08-802-805D-6
22	1120.5	45.0	464	4	US-08-861-990-2
23	1117.5	44.9	464	4	US-09-388-316C-6
24	1117.5	44.9	464	3	US-08-957-063-3
25	1117.5	44.9	464	3	US-09-487-685-3
26	1117.5	44.9	464	3	US-08-802-805D-3
27	1109.5	44.6	464	4	US-09-388-316C-13
					Sequence 13, Appl

28	1108.5	44.6	464	4	US-08-861-990-9	Sequence 9, Appl
29	1100	44.2	664	3	US-08-957-063-18	Sequence 18, Appl
30	1100	44.2	664	3	US-09-487-685-18	Sequence 18, Appl
31	1100	44.2	664	3	US-08-802-805D-18	Sequence 18, Appl
32	1100	44.2	664	4	US-09-388-316C-18	Sequence 18, Appl
33	1099.5	44.2	664	3	US-08-957-063-16	Sequence 16, Appl
34	1099.5	44.2	664	3	US-09-487-685-16	Sequence 16, Appl
35	1099.5	44.2	664	3	US-08-802-805D-16	Sequence 16, Appl
36	1099.5	44.2	664	4	US-09-388-316C-16	Sequence 16, Appl
37	1098.5	44.2	445	4	US-08-861-990-11	Sequence 11, Appl
38	1098.5	44.2	445	4	US-08-837-199A-18	Sequence 18, Appl
39	983.5	39.5	209	4	US-08-837-199A-20	Sequence 20, Appl
40	646.5	26.0	147	4	US-08-837-199A-22	Sequence 22, Appl
41	617.5	24.8	141	4	US-08-837-199A-24	Sequence 24, Appl
42	511	20.5	400	3	US-09-220-528-63	Sequence 63, Appl
43	511	20.5	400	3	US-09-187-906-21	Sequence 21, Appl
44	511	20.5	400	4	US-09-494-016-9079	Sequence 9079, Ap
45	505.5	20.3	397	3	US-09-220-528-64	Sequence 64, Appl

ALIGNMENTS

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RESULT 1
US-08-802-805D-21
Sequence 21, Application US/08802805D
Patent No. 6372453
GENERAL INFORMATION:
APPLICANT: Robert D. Klein
TITLE OF INVENTION: Neuturin Receptor
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802, 805D
FILING DATE: 18-Feb-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-802-805D-21
Query Match 100.0%; Score 2488; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB SLTSGLEADCEGSAEALKOKSLVNCRCRKGKKEKNCRLRIYMSYQSLQGNLLDSDP 120

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Db 361 QTTTATTTTARVKNKPLGPGAGSENEIPTHVLPCCANLQAQKLSNVSGSTHLCISDSDF 420
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QY 421 GKDGLAGASHITTKSMAPPCSSLPVLM/LTALAALLSVSLAETS 468
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Db 421 GKDGLAGASHITTKSMAPPCSSLPVLM/LTALAALLSVSLAETS 468
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RESULT 2

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US-08-837-199A-4
; Sequence 4, Application US/08837199A
; Patent No. 6453277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: MEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837.199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; LENGTH: 468
; TYPE: PRT
; ORGANISM: RAT
US-08-837-199A-4

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Query Match 100.0%; Score 2488; DB 4; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5,1e-233;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNKCLDAKACNLDPTCKKRSAYITPCTT 180
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Db 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNKCLDAKACNLDPTCKKRSAYITPCTT 180
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Db 181 SMSNEVCNRRKCHALROFPDKVPKSHSYGMLFCSCRDIACTERRRQITVPCSYEEBR 240
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Db 241 PNCISLQDSCKTNYICRSRLADFTNQCPSRSVSNCLKENYADCLLAYSGLIGVMTPN 300
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Db 361 QTTTATTTTARVKNKPLGPGAGSENEIPTHVLPCCANLQAQKLSNVSGSTHLCISDSDF 420
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|
|
QY 421 GKDGLAGASHITTKSMAPPCSSLPVLM/LTALAALLSVSLAETS 468
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Db 421 GKDGLAGASHITTKSMAPPCSSLPVLM/LTALAALLSVSLAETS 468
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RESULT 3

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US-08-860-370-2
; Sequence 2, Application US/08860370
; Patent No. 6504007
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Klein, Robert D.
; APPLICANT: Moore, Mark W.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Ryan, Anne M.
; TITLE OF INVENTION: USES OF GDNF AND GDNF RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

```

COMPUTER READABLE FORM:

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MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04363
FILING DATE: 13-Mar-1997
APPLICATION NUMBER: 08/615902
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618236
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0996P1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9874
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: Extracellular Domain
LOCATION: 25
IDENTIFICATION METHOD:
OTHER INFORMATION:
NAME/KEY: Mature Protein N-terminal
LOCATION: 25-427
IDENTIFICATION METHOD:
OTHER INFORMATION:
NAME/KEY: Potential Glycosylation Site

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LOCATION: 349
IDENTIFICATION METHOD:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Potential Glycosylation Site
LOCATION: 408
IDENTIFICATION METHOD:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Potential Glycosylation Site
LOCATION: 61
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-860-370-2

Query Match      100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SLTSGLEAKDECSAMEALQKSLVNCRCRKGKKEKNCRIYWSMYQSLQNDLLEDS 120
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DB 121 YEPVNSRLSDIFRAVFIIDVFOVEHISKNNCLDAKACNLDITCKKYSAYITPCTT 180
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DB 301 YVDSLSLVAWPCDCNSGNDLEDCLEFLNFFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
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DB 361 QTTTATTTTAFRYKKNRPLGPGASENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSDF 420
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DB 421 GKXGLAGASSHITTKSMAPPSCSLSLPLVMTALALISVLAETS 468

RESULT 4
US-09-187-906-2
Sequence 2, Application US/09187906
Patent No. 6677135
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
TITLE OF INVENTION: and Renal Growth
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/187, 906
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-187-906-2

Query Match      100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATLYFALPLDLMSAEVSGGDRDLCYKASDOCLKEOSCTKRTTLQCVAGKETNF 60
DB 1 MFATLYFALPLDLMSAEVSGGDRDLCYKASDOCLKEOSCTKRTTLQCVAGKETNF 60
QY 61 SLTSGLEAKDECSAMEALQKSLVNCRCRKGKKEKNCRIYWSMYQSLQNDLLEDS 120
DB 61 SLTSGLEAKDECSAMEALQKSLVNCRCRKGKKEKNCRIYWSMYQSLQNDLLEDS 120
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DB 121 YEPVNSRLSDIFRAVFIIDVFOVEHISKNNCLDAKACNLDITCKKYSAYITPCTT 180
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DB 121 YEPVNSRLSDIFRAVFIIDVFOVEHISKNNCLDAKACNLDITCKKYSAYITPCTT 180
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DB 181 SMNEVCNRRKCHKALRQFPDKVPAGSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
QY 181 SMNEVCNRRKCHKALRQFPDKVPAGSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMNEVCNRRKCHKALRQFPDKVPAGSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
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DB 241 PNCLSLDSCCTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLAYSGLIGTWTPN 300
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DB 301 YVDSLSLVAWPCDCNSGNDLEDCLEFLNFFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
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DB 361 QTTTATTTTAFRYKKNRPLGPGASENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSDF 420
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DB 421 GKXGLAGASSHITTKSMAPPSCSLSLPLVMTALALISVLAETS 468

RESULT 5
US-08-861-990-1
Sequence 1, Application US/08861990
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/ Patent No. 6696259
/ GENERAL INFORMATION:
/ APPLICANT: Idenez, Carlos F.
/ APPLICANT: Arumae, Umas
/ APPLICANT: Sariola, Hannu
/ APPLICANT: Savanto, Petro
/ APPLICANT: Trupp, Miles
/ APPLICANT: Saarna, Mart
/ TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor Receptors
/ FILE REFERENCE: CEPH0418
/ CURRENT APPLICATION NUMBER: US/08/861,990
/ PRIOR FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: 08/747,842
/ PRIOR FILING DATE: 1996-11-13
/ PRIOR APPLICATION NUMBER: 60/006,619
/ PRIOR FILING DATE: 1995-11-13
/ PRIOR APPLICATION NUMBER: 60/015,767
/ PRIOR FILING DATE: 1996-04-16
/ PRIOR APPLICATION NUMBER: 60/021,965
/ PRIOR FILING DATE: 1996-06-27
/ PRIOR APPLICATION NUMBER: 60/020,638
/ PRIOR FILING DATE: 1996-06-27
/ PRIOR APPLICATION NUMBER: 60/020,639
/ PRIOR FILING DATE: 1996-06-27
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 468
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ US-08-861-990-1
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Query Match          100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5,1e-23; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;
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QY 1 MFATLYPALPLDLILMSAEVSGDRLDVCVKSDDCKEKGSCSTKYRTLQCVAGKETNF 60
DB 1 MFATLYPALPLDLILMSAEVSGDRLDVCVKSDDCKEKGSCSTKYRTLQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGMKKEKNCRLIYWSMYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGMKKEKNCRLIYWSMYOSLGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAAKCNLDCTCKYRSAYITPCTT 180
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QY 181 SMSNEVCNRKCHKALROFDFKVPKHSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
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DB 301 YVDSLSLVAWPCDCSNGNDLEDCIKPLNFKONTCLKNAIOARNGSDVTMMQAPAPV 360
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DB 361 OTTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANIOAKLKSNVSGSTHCLSDSDF 420
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DB 421 GKDGAGASSHTTTKSMAPPCSSLSLPVLMITLALALSVSLAETS 468
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RESULT 6
US-09-388-316C-21
; Sequence 21, Application US/09388316C
; Patent No. 6777196
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/ GENERAL INFORMATION:
/ APPLICANT: KLEIN, ROBERT D.
/ APPLICANT: ROSENTHAL, ARNON
/ APPLICANT: HYNES, MARY A.
/ TITLE OF INVENTION: NEURTURIN RECEPTOR
/ FILE REFERENCE: GENENT.45A2DV1
/ CURRENT APPLICATION NUMBER: US/09/388,316C
/ CURRENT FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: 09/024,665
/ PRIOR FILING DATE: 1998-02-17
/ PRIOR APPLICATION NUMBER: 60/063,258
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/049,818
/ PRIOR FILING DATE: 1997-06-09
/ PRIOR APPLICATION NUMBER: 60/038,839
/ PRIOR FILING DATE: 1997-02-18
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 468
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ US-09-388-316C-21
```

```
Query Match          100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5,1e-23; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;
```

```
QY 1 MFATLYPALPLDLILMSAEVSGDRLDVCVKSDDCKEKGSCSTKYRTLQCVAGKETNF 60
DB 1 MFATLYPALPLDLILMSAEVSGDRLDVCVKSDDCKEKGSCSTKYRTLQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGMKKEKNCRLIYWSMYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGMKKEKNCRLIYWSMYOSLGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAAKCNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAAKCNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFDFKVPKHSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRKCHKALROFDFKVPKHSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
QY 241 PNCISLQDSCKTNYICRSLADPFTNCOPESSRSVSNCKENYADCLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSLADPFTNCOPESSRSVSNCKENYADCLAYSGLIGVTMPN 300
QY 301 YVDSLSLVAWPCDCSNGNDLEDCIKPLNFKONTCLKNAIOARNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAWPCDCSNGNDLEDCIKPLNFKONTCLKNAIOARNGSDVTMMQAPAPV 360
QY 361 OTTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANIOAKLKSNVSGSTHCLSDSDF 420
DB 361 OTTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANIOAKLKSNVSGSTHCLSDSDF 420
QY 421 GKDGAGASSHTTTKSMAPPCSSLSLPVLMITLALALSVSLAETS 468
DB 421 GKDGAGASSHTTTKSMAPPCSSLSLPVLMITLALALSVSLAETS 468
```

```
RESULT 7
US-08-837-199A-2
; Sequence 2, Application US/08837199A
; Patent No. 6455277
/ GENERAL INFORMATION:
/ APPLICANT: FOX, GARY M.
/ APPLICANT: JING, SHUOIAN
/ APPLICANT: MEN, DIANZHI
/ TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
/ FILE REFERENCE: A-401C
/ CURRENT APPLICATION NUMBER: US/08/837,199A
/ CURRENT FILING DATE: 1997-04-14
```

PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 465
TYPE: PR
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
NAME/KEY: misc feature
LOCATION: (2107)..(2107)
OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
NAME/KEY: misc feature
LOCATION: (2241)..(2241)
OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
NAME/KEY: misc feature
LOCATION: (2250)..(2250)
OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
NAME/KEY: misc feature
LOCATION: (2256)..(2256)
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be
OTHER INFORMATION: tween different receptor clones
US-08-837-199A-2

Query Match 93.1%; Score 2316.5; DB 4; Length 465;
Best Local Similarity 92.7%; Pred. No. 2,4e-216;
Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 MFATLYFALPLDILMSAEVSGDRLDCVKASDQCKEOSTKRTLRQCVAGKETNF 60
DB 1 MFATLYFALPLDILMSAEVSGDRLDCVKASDQCKEOSTKRTLRQCVAGKETNF 60
QY 61 SLTSGLEADDECSAMEALKQKSLYNCRCKRGKKEKNCRIYMSYQSLQGNLDLEDSP 120
DB 61 SLTSGLEADDECSAMEALKQKSLYNCRCKRGKKEKNCRIYMSYQSLQGNLDLEDSP 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCHKALRQFPDKVPAKHSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
DB 181 SVSNDVCNRRKCHKALRQFPDKVPAKHSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YVDSLSLVAPWMDCSNGNDLEDCIKFLNFKDNTCLKNAIOAFNGSDVTWQAPAPV 360
DB 301 YVDSLSLVAPWMDCSNGNDLEDCIKFLNFKDNTCLKNAIOAFNGSDVTWQAPAPV 360
QY 361 QTTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAKLSNVSGTTHCLSDSDF 420
DB 361 QTTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAKLSNVSGTTHCLSDSDF 420
QY 421 GKDLGASGSHITTKSMAAPSCSLSLPLVMTALAAISVLAETS 468
DB 421 EKXGL-GASSHITTKSMAAPSCSLPLVLVLTALSTLL--SLTETS 465

RESULT 8
US-09-388-316C-22
Sequence 22, Application US/09388316C

Patent No. 6777196
GENERAL INFORMATION:
APPLICANT: KLEIN, ROBERT D.
APPLICANT: ROSENTHAL, ARNON
APPLICANT: HYNES, MARY A.
TITLE OF INVENTION: NEURTURIN RECEPTOR
FILE REFERENCE: GENENT.45A2DV1
CURRENT APPLICATION NUMBER: US/09/388,316C
CURRENT FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: 09/024,665
PRIOR FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 60/063,258
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/049,818
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: 60/038,839
PRIOR FILING DATE: 1997-02-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 465
TYPE: PR
ORGANISM: Homo sapiens
US-09-388-316C-22

Query Match 93.1%; Score 2316.5; DB 4; Length 465;
Best Local Similarity 92.7%; Pred. No. 2,4e-216;
Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 MFATLYFALPLDILMSAEVSGDRLDCVKASDQCKEOSTKRTLRQCVAGKETNF 60
DB 1 MFATLYFALPLDILMSAEVSGDRLDCVKASDQCKEOSTKRTLRQCVAGKETNF 60
QY 61 SLTSGLEADDECSAMEALKQKSLYNCRCKRGKKEKNCRIYMSYQSLQGNLDLEDSP 120
DB 61 SLTSGLEADDECSAMEALKQKSLYNCRCKRGKKEKNCRIYMSYQSLQGNLDLEDSP 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCHKALRQFPDKVPAKHSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
DB 181 SVSNDVCNRRKCHKALRQFPDKVPAKHSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YVDSLSLVAPWMDCSNGNDLEDCIKFLNFKDNTCLKNAIOAFNGSDVTWQAPAPV 360
DB 301 YVDSLSLVAPWMDCSNGNDLEDCIKFLNFKDNTCLKNAIOAFNGSDVTWQAPAPV 360
QY 361 QTTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAKLSNVSGTTHCLSDSDF 420
DB 361 QTTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAKLSNVSGTTHCLSDSDF 420
QY 421 GKDLGASGSHITTKSMAAPSCSLSLPLVMTALAAISVLAETS 468
DB 421 EKXGL-GASSHITTKSMAAPSCSLPLVLVLTALSTLL--SLTETS 465

RESULT 9
US-08-837-199A-12
Sequence 12, Application US/08837199A
Patent No. 6455277
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/08/837,199A

;; CURRENT FILING DATE: 1997-04-14
;; PRIOR APPLICATION NUMBER: US 60/015,907
;; PRIOR FILING DATE: 1996-04-22
;; PRIOR APPLICATION NUMBER: US 60/017,221
;; PRIOR FILING DATE: 1996-05-09
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 12
;; LENGTH: 463
;; TYPE: PRT
;; ORGANISM: HUMAN
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(539)
;; OTHER INFORMATION: No. 64552776= "1 to 539 is -237 to 301 of Figure 5 21bcon"
US-08-837-199A-12

Query Match 92.9%; Score 2311.5; DB 4; Length 463;
Best Local Similarity 92.9%; Pred. No. 7.2e-216;
Matches 430; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

```
QY 1 MFATLYPALPLDLMSAEVSGGDRLDVCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
DB 1 MFATLYPALPLDLMSAEVSGGDRLDVCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
DB 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI SKNNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
DB 181 SMSNEVCNRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
QY 181 SVSNDVCCRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
DB 181 SVSNDVCCRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
QY 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
DB 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
QY 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
DB 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
QY 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
DB 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
QY 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
DB 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
QY 421 GKDLGAGSSHITTKSMAAPSCSLSLPVLMLTALAALLSVS 463
DB 421 GKDLGAGSSHITTKSMAAPSCSLSLPVLMLTALAALLSVS 463
QY 421 EKEGL-GASSHITTKSMAAPSCSLPLVLVVTALSTLLST 462
DB 421 EKEGL-GASSHITTKSMAAPSCSLPLVLVVTALSTLLST 462
```

RESULT 10
US-08-861-990-8
;; Sequence 8, Application US/08861990
;; Patent No. 6696259
;; GENERAL INFORMATION:
;; APPLICANT: Ibanez, Carlos F.
;; APPLICANT: Arumae, Umas
;; APPLICANT: Sarioia, Hannu
;; APPLICANT: Suvanto, Petro
;; APPLICANT: Trupp, Miles
;; APPLICANT: Saarna, Mart
;; TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor Receptors
;; FILE REFERENCE: CEPH0418
;; CURRENT APPLICATION NUMBER: US/08/861,990
;; PRIOR FILING DATE: 1997-05-22
;; PRIOR APPLICATION NUMBER: 08/747,842
;; PRIOR FILING DATE: 1996-11-13
;; PRIOR APPLICATION NUMBER: 60/006,619
;; PRIOR FILING DATE: 1995-11-13

;; PRIOR APPLICATION NUMBER: 60/015,767
;; PRIOR FILING DATE: 1996-04-16
;; PRIOR APPLICATION NUMBER: 60/021,965
;; PRIOR FILING DATE: 1996-06-27
;; PRIOR APPLICATION NUMBER: 60/020,638
;; PRIOR FILING DATE: 1996-06-27
;; PRIOR APPLICATION NUMBER: 60/020,639
;; PRIOR FILING DATE: 1996-06-27
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 465
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-861-990-8

Query Match 92.9%; Score 2310.5; DB 4; Length 465;
Best Local Similarity 92.5%; Pred. No. 9e-216;
Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

```
QY 1 MFATLYPALPLDLMSAEVSGGDRLDVCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
DB 1 MFATLYPALPLDLMSAEVSGGDRLDVCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
DB 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI SKNNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
DB 181 SMSNEVCNRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
QY 181 SVSNDVCCRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
DB 181 SVSNDVCCRKCHKALRQFPDKVPKASHYGMFCSCRDIACTERRRQTIYPVCSYEERER 240
QY 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
DB 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
QY 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
DB 241 PNCNLSQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLLAYSGLIGVTWTPN 300
QY 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSSSLVAWCCCSNGNDLEDCIKFNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
DB 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
QY 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
DB 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAOQKLSNVSGSTHLCISDSDF 420
QY 421 GKDLGAGSSHITTKSMAAPSCSLSLPVLMLTALAALLSVS 468
DB 421 GKDLGAGSSHITTKSMAAPSCSLSLPVLMLTALAALLSVS 468
QY 421 EKEGL-GASSHITTKSMAAPSCSLPLVLVVTALSTLL--SLTETS 465
DB 421 EKEGL-GASSHITTKSMAAPSCSLPLVLVVTALSTLL--SLTETS 465
```

RESULT 11
US-08-837-199A-6
;; Sequence 6, Application US/08837199A
;; Patent No. 6455277
;; GENERAL INFORMATION:
;; APPLICANT: FOX, GARY M.
;; APPLICANT: JING, SHUOJIAN
;; APPLICANT: WEN, DUANZHI
;; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
;; FILE REFERENCE: A-401C
;; CURRENT APPLICATION NUMBER: US/08/837,199A
;; PRIOR FILING DATE: 1997-04-14
;; PRIOR APPLICATION NUMBER: US 60/015,907
;; PRIOR FILING DATE: 1996-04-22
;; PRIOR APPLICATION NUMBER: US 60/017,221
;; PRIOR FILING DATE: 1996-05-09
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 465

TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (184)..(184)
OTHER INFORMATION: The 'Xaa' at location 184 stands for Lys, or Asn.
NAME/KEY: misc feature
LOCATION: (1)..(510)
OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hegr-21bf"
NAME/KEY: misc feature
LOCATION: (1)..(539)
OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
NAME/KEY: misc feature
LOCATION: (2256)..(2294)
OTHER INFORMATION: N in position 2256 to 2294 indicates positions of divergence bet
OTHER INFORMATION: ween different receptor clones
NAME/KEY: misc feature
LOCATION: (1091)..(1091)
OTHER INFORMATION: N in position 1091 indicates any nucleic acid
US-08-837-199A-6

Query Match 92.8%; Score 2309.5; DB 4; Length 465;
Best Local Similarity 92.5%; Pred. No. 1.1e-215;
Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

QY 1 MFLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKYRTLRQCVAGKETNF 60
DB 1 MFLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKYRTLRQCVAGKETNF 60
QY 61 SLTSGLEADECBSAMEALKOKSLYNCRCKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
DB 61 SLTSGLEADECBSAMEALKOKSLYNCRCKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
QY 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCKHAKLROFPDKVPAKHSYGMLFCSGRDIACCTERRRQTIYPVCSYERER 240
DB 181 SMSNEVCNRRKCKHAKLROFPDKVPAKHSYGMLFCSGRDIACCTERRRQTIYPVCSYERER 240
QY 241 PNCLSLQDSCKTYICRSRLADFTNCOPESSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTYICRSRLADFTNCOPESSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YDSSSLVAAPWCDCSNGNDLEDCIKFLNFPKONTCLKNAIOAFNGSDVTWOPAPV 360
DB 301 YDSSSLVAAPWCDCSNGNDLEDCIKFLNFPKONTCLKNAIOAFNGSDVTWOPAPV 360
QY 361 QTTTATTTAFAFRKNPLGPAGSENEIPTHVLPPCANLQAKLKSXVSGSTHCLSDSP 420
DB 361 QTTTATTTAFAFRKNPLGPAGSENEIPTHVLPPCANLQAKLKSXVSGSTHCLSDSP 420
QY 421 GKDGLAGASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 468
DB 421 GKDGLAGASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 468
QY 421 EKEGL-GASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 465
DB 421 EKEGL-GASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 465

RESULT 12
US-08-837-199A-10
Sequence 10, Application US/08837199A
Patent No. 6455277
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHOUJIAN
APPLICANT: WEN, DUANZHIT
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/08/837, 199A

CURRENT FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015, 907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017, 221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 463
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: The 'Xaa' at location 5 stands for Thr, Ala, Pro, or Ser.
NAME/KEY: misc feature
LOCATION: (1)..(537)
OTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
NAME/KEY: misc feature
LOCATION: (550)..(550)
OTHER INFORMATION: N in position 550 indicates any nucleic acid
US-08-837-199A-10

Query Match 92.7%; Score 2306.5; DB 4; Length 463;
Best Local Similarity 92.7%; Pred. No. 2.2e-215;
Matches 429; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 1 MFLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKYRTLRQCVAGKETNF 60
DB 1 MFLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKYRTLRQCVAGKETNF 60
QY 61 SLTSGLEADECBSAMEALKOKSLYNCRCKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
DB 61 SLTSGLEADECBSAMEALKOKSLYNCRCKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
QY 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIFRAVPFISDVFOOVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCKHAKLROFPDKVPAKHSYGMLFCSGRDIACCTERRRQTIYPVCSYERER 240
DB 181 SMSNEVCNRRKCKHAKLROFPDKVPAKHSYGMLFCSGRDIACCTERRRQTIYPVCSYERER 240
QY 241 PNCLSLQDSCKTYICRSRLADFTNCOPESSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTYICRSRLADFTNCOPESSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YDSSSLVAAPWCDCSNGNDLEDCIKFLNFPKONTCLKNAIOAFNGSDVTWOPAPV 360
DB 301 YDSSSLVAAPWCDCSNGNDLEDCIKFLNFPKONTCLKNAIOAFNGSDVTWOPAPV 360
QY 361 QTTTATTTAFAFRKNPLGPAGSENEIPTHVLPPCANLQAKLKSXVSGSTHCLSDSP 420
DB 361 QTTTATTTAFAFRKNPLGPAGSENEIPTHVLPPCANLQAKLKSXVSGSTHCLSDSP 420
QY 421 GKDGLAGASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 463
DB 421 GKDGLAGASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 462
QY 421 EKEGL-GASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 462
DB 421 EKEGL-GASSHTTTKMAAPPCSSLSLPLYMLTALAALSVLSAETS 462

RESULT 13
US-08-802-805D-22
Sequence 22, Application US/08802805D
Patent No. 6372453
GENERAL INFORMATION:
APPLICANT: Robert D. Klein
TITLE OF INVENTION: Neurturin Receptor
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,805D
FILING DATE: 18-Feb-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-802-805D-22

Query Match 91.6%; Score 2278; DB 3; Length 460;
Best Local Similarity 91.7%; Pred. No. 1.3e-212;
Matches 429; Conservative 18; Mismatches 13; Indels 8; Gaps 3;

QY 1 MFLLATYFALPLDLILMSAEVSGGDRIDCVKASDQCLKEQSCSTKYRTLRCVAGKETNF 60
DB 1 MFLLATYFALPLDLILMSAEVSGGDRIDCVKASDQCLKEQSCSTKYRTLRCVAGKETNF 60
QY 61 SLTSGLEAKDCRSMELKOKSLYNCRCKRMKEKNCRLRYMSWYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSMELKOKSLYNCRCKRMKEKNCRLRYMSWYOSLGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLRQFDFKVPKASGYGLFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRRCKHAKLRQFDFKVPKASGYGLFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCLSLDSCSKTNYICSRRLADFTNCOPESSRSVSNCLKENYADCLLAISGLIGVTWTPN 300
DB 241 PNCLSLDSCSKTNYICSRRLADFTNCOPESSRSVSNCLKENYADCLLAISGLIGVTWTPN 300
QY 301 YVDSLSLSVAWPCDSCNSGNDLEDCLEKLFNFKONTCLKNAIOAFGNSGVYTMQAPAPV 360
DB 301 YVDSLSLSVAWPCDSCNSGNDLEDCLEKLFNFKONTCLKNAIOAFGNSGVYTMQAPAPV 360
QY 361 QTTATTTTARVKNKPLGPAAGSENEIPTHVLPICANTAOQCLKSNVSGSTHLCISDSDF 420
DB 361 QTTATTTTARVKNKPLGPAAGSENEIPTHVLPICANTAOQCLKSNVSGSTHLCISDSDF 420
QY 421 GKDGAGAGSHITTKSMAPPSCSLPLVLTALALSLAETS 468
DB 421 GKDGAGAGSHITTKSMAPPSCSLPLVLTALALSLAETS 468

RESULT 14

US-09-187-906-11
Sequence 11, Application US/09187906
Patent No. 6677135
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
TITLE OF INVENTION: and Renal Growth
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/187,906
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-187-906-11

Query Match 91.6%; Score 2278; DB 4; Length 460;
Best Local Similarity 91.7%; Pred. No. 1.3e-212;
Matches 429; Conservative 18; Mismatches 13; Indels 8; Gaps 3;

QY 1 MFLLATYFALPLDLILMSAEVSGGDRIDCVKASDQCLKEQSCSTKYRTLRCVAGKETNF 60
DB 1 MFLLATYFALPLDLILMSAEVSGGDRIDCVKASDQCLKEQSCSTKYRTLRCVAGKETNF 60
QY 61 SLTSGLEAKDCRSMELKOKSLYNCRCKRMKEKNCRLRYMSWYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSMELKOKSLYNCRCKRMKEKNCRLRYMSWYOSLGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLRQFDFKVPKASGYGLFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRRCKHAKLRQFDFKVPKASGYGLFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCLSLDSCSKTNYICSRRLADFTNCOPESSRSVSNCLKENYADCLLAISGLIGVTWTPN 300
DB 241 PNCLSLDSCSKTNYICSRRLADFTNCOPESSRSVSNCLKENYADCLLAISGLIGVTWTPN 300
QY 301 YVDSLSLSVAWPCDSCNSGNDLEDCLEKLFNFKONTCLKNAIOAFGNSGVYTMQAPAPV 360
DB 301 YVDSLSLSVAWPCDSCNSGNDLEDCLEKLFNFKONTCLKNAIOAFGNSGVYTMQAPAPV 360
QY 361 QTTATTTTARVKNKPLGPAAGSENEIPTHVLPICANTAOQCLKSNVSGSTHLCISDSDF 420
DB 361 QTTATTTTARVKNKPLGPAAGSENEIPTHVLPICANTAOQCLKSNVSGSTHLCISDSDF 420

Db 356 QTTTATTATLRYKNKPLGPGAGSENEIPTHVLPCCANLQAOXKLSNVSGNTHLCISNGNY 415

QY 421 GKGLAGASHITTKSMAAPPSCSLSPVLMTLTALALISVLAETS.468

Db 416 EKEGL-GASSHITTKSMAAPPSCSLSPVLVLTALSTLL-SLETFS 460

RESULT 15

US-09-187-906-9

Sequence 9, Application US/09187906

Patent No. 6677135

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.

TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural

TITLE OF INVENTION: and Renal Growth

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02142

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/187,906

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/07726

FILING DATE: 07-MAY-97

APPLICATION NUMBER: US 60/017,427

FILING DATE: 08-MAY-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/019,300

FILING DATE: 07-JUN-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/021,859

FILING DATE: 16-JUL-96

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043,533

FILING DATE: 10-APR-97

ATTORNEY/AGENT INFORMATION:

NAME: Kaplan, Warren A.

REGISTRATION NUMBER: 34,199

REFERENCE/DOCKET NUMBER: A008 PCT CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-679-2400

TELEFAX: 617-679-2838

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 346 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-187-906-9

Query Match

Best Local Similarity 89.5%; Score 1686; DB 4; Length 346;

Matches 317; Conservative 17; Mismatches 12; Indels 8; Gaps 3;

QY 115 LLEDSYEPNLSLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAY 174

Db 1 LLEDSYEPNLSLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAY 55

QY 175 ITPECTTSMNSVNCRRKCHALROFPDKVPAKHSYGLFSCSRDIACCTERRRQTIIVPCS 234

Db 56 ITPECTTSMNSVNCRRKCHALROFPDKVPAKHSYGLFSCSRDIACCTERRRQTIIVPCS 115

QY 235 YERERPNCLSLDSCSKTYICRSRLADFPNCPBSRSVSNCLXENYADCLLAYSGILG 294

Db 116 YERERPNCLSLDSCSKTYICRSRLADFPNCPBSRSVSNCLXENYADCLLAYSGILG 175

QY 295 TVMTPNYVDSSSLVAPMCDSCNSGNDLEDCLEFNFKONTCLKNAIQAFNGSDVTW 354

Db 176 TVMTPNYVDSSSLVAPMCDSCNSGNDLEDCLEFNFKONTCLKNAIQAFNGSDVTW 235

QY 355 QPAPVQTTTATTATTAFRVKNKPLGPGAGSENEIPTHVLPCCANLQAOXKLSNVSGNTHLC 414

Db 236 QPAPVQTTTATTATTAFRVKNKPLGPGAGSENEIPTHVLPCCANLQAOXKLSNVSGNTHLC 295

QY 415 LSDSDFGKGLAGASHITTKSMAAPPSCSLSPVLMTLTALALISVLAETS 468

Db 296 ISNGYEKGL-GASSHITTKSMAAPPSCSLSPVLVLTALSTLL-SLETFS 346

Search completed: February 17, 2005, 09:49:08
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:13 ; Search time 44 Seconds
(without alignments)
1023.396 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488
Sequence: 1 MFLATLYRALPLDLLMSAE.....PYLMLTALAALLSVSLAETS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505.5	20.3	397	2 JE0082	GPI-linked receptor
2	148	5.9	3051	2 S42373	hypothetical prote
3	131	5.3	2471	2 A49128	cell-fate determin
4	129	5.2	2700	2 S04847	leukocyte adhesion
5	129	5.2	2703	1 A24420	notch protein - tr
6	128	5.1	771	2 A45639	leukocyte adhesion
7	127.5	5.1	601	2 B36346	fibulin 1 precursor
8	125.5	5.0	2139	2 A35672	crumbs protein - f
9	125	5.0	2195	2 S62935	hypothetical prote
10	123.5	5.0	2195	2 T34264	hypothetical prote
11	121.5	4.9	810	2 T10756	Nel-homolog protei
12	121.5	4.9	886	2 A57172	probable hormone r
13	121	4.9	683	2 C36346	fibulin 1 precursor
14	121	4.9	1292	2 T09229	galactose binding
15	120	4.8	2531	2 T31070	notch homolog - se
16	119.5	4.8	1051	2 JC4091	glycoprotein A - p
17	119.5	4.8	3507	2 T34513	hypothetical prote
18	119	4.8	685	2 S78040	fibulin, splice fo
19	119	4.8	705	2 S34968	LDL-receptor-relac
20	119	4.8	4753	1 A47437	major surface glyco
21	117.5	4.7	715	2 JC2222	Notch B protein -
22	117	4.7	1203	2 A49175	alpha-2-macroglobu
23	116.5	4.7	4543	1 A53102	GDNF receptor alpa
24	116	4.7	24	2 S69080	notch protein - chlc
25	115.5	4.6	835	2 JP0076	G surface protein
26	115.5	4.6	2704	2 S09118	surface protein ty
27	115	4.6	2395	2 S50820	alpha-5ID immobill
28	114.5	4.6	2533	2 T28675	alpha-5ID-immobill
29	114.5	4.6	2533	2 T28674	alpha-5ID-immobill

30	113	4.5	1599	2 T16210	hypothetical prote
31	111.5	4.5	1722	2 B89753	protein FltC7.4 (l
32	111.5	4.5	2643	2 T29149	hypothetical prote
33	111.5	4.5	2718	2 A23475	G surface protein
34	111	4.5	600	2 S07638	spore coat protein
35	110.5	4.4	907	2 T27317	hypothetical prote
36	110	4.4	2437	2 S42612	transmembrane prot
37	109.5	4.4	5376	2 T42215	zonadhesin - mouse
38	109	4.4	2524	2 A35844	Xotch protein - Af
39	108.5	4.4	1169	2 S31811	filocolation prote
40	108	4.3	1142	2 T30272	hypothetical prote
41	107	4.3	1004	2 JC2221	major surface glyco
42	107	4.3	1296	2 T16859	hypothetical prote
43	106.5	4.3	332	2 T21458	hypothetical prote
44	106.5	4.3	1927	2 G64585	cag pathogenicity
45	106.5	4.3	2233	2 T28669	surface protein 51

ALIGNMENTS

```

RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N/Alternate names: GFRalpha-3
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: JE0082
R/Nomoto, S.; Ito, S.; Yang, L.X.; Kluich, K.
Biochem. Biophys. Res. Commun. 244, 849-851, 1998
A/Title: Molecular cloning and expression analysis of GFRalpha-3, a novel CDNA related to
A/Reference number: JE0082; MUID:98205811; PMID:9535755
A/Accession: JE0082
A/Molecule type: mRNA
A/Residues: 1-397 <NOM>
A/Cross-references: UNIPROT:035118; DDBJ:AB008833; NID:92627159; PIDD:BAA23562.1; PTD:92
C/Comment: This protein plays a distinct role in cell survival and differentiation.
C/Superfamily: Mus musculus GPI-linked receptor
C/Keywords: glycoprotein
F/1-25/Domain: signal sequence #status predicted <SIG>
F/380-397/Region: hydrophobic
F/92,145,306/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match      20.3%; Score 505.5; DB 2; Length 397;
Best Local Similarity 35.1%; Pred. No. 2.6e-30;
Matches 125; Conservative 40; Mismatches 148; Indels 43; Gaps 12;

QY 11 PLDLLMSA-----EYSGGDRL-----DVKASDQCLKQSGSTKYRTLRQVAKGE 57
DB 10 PLMLTLLVLSLWPLPGAGNSLATENRFVNSCTQARKKEANPACAAVOHLGSCSTSSLS 69
QY 58 TWFSLTSGLEAKDECSAREALKQSLVNCRCRGKKKCNCLRIYWSYQSIQ-GNDLL 116
DB 70 RPLPLESAMSAD-CLEAAEQRLNSLIDCRCHRRKQATCLDIYWTYHAPASLDYEL 128
QY 117 EDSPYE-----PVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDTCCKY 170
DB 129 DSPYEDVTYSKPKWKNLSKLNMLKP-DSDL-----CLFPMILCTLHDCDLRL 175
QY 171 RSAVITPCTSMNSNEVONRKCHKALROFPEDVPKAGSYGMFCSC--RDIACTERRROT 228
DB 176 RKAHYGEA---SGIRCOHLLCLAQIRSFPEKAESHAGLLCPAPEDAGGERRRNT 231
QY 229 IYVVCSEERERPNCLSDSCCTNYICSRILADFPFTNOCPESSRSVNCLEKNYADCLLA 288
DB 232 IAPSCALPS-VTPNCGLDASPCRADPLGSRMLDPFTHCHPMD-IIGTCATGQ-SRCLRA 288
QY 289 YSGLICTVTPYVNDSSLSVAPWCDSCNSGNDLEDCLKFLNFKQNTCLKAIOA 344
DB 289 YGLIGTAMTPNFIKSVNTTVALSCTCRGSGNLODECEQLERSFSQNPCLVEAIIA 344

```

RESULT 2

S42373

hypothetical protein T20G5.3 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004

C/Accession: S42373

R:Smith, A.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42368

A/Accession: S42373

A/Molecule type: DNA

A/Residues: 1-3051 <SMI>

A/Cross-references: EMBL:Z30423; NID:G458479; PID:G458485

C/Genetics: A:Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;

F:512-679/Domain: von Willebrand factor type A repeat homology <WAL>

F:754-793/Domain: fibronectin type II repeat homology <2FI>

F:1201-1244/Domain: EGF homology <EGF>

Query Match 5.9%; Score 148; DB 2; Length 3051;
 Best Local Similarity 18.3%; Pred. No. 0.017;
 Matches 97; Conservative 49; Mismatches 158; Indels 226; Gaps 24;

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QY 36 CLKRQSC-STYKRTLRQCV-----AGKTNFSLTSGLEAKDECRSANEALQ 81
Db 7 CAABAECEETPIGMCCQGVYDVSROHGRPAQVAVNECAEGHHDSSHTCIDT 66
QY 82 KSLYNCRCKRMKE-----KNCIRIYMSWYQSLQGN-----DLLEDSEYEVN--- 125
Db 67 ADEFTCRCKDSYRDESSDTLKHPRGNVCR-----TVQPRPECDVDSDPSCDAKEV 119
QY 126 -----SRLSDIFRAVPFISDFQGVENHISKNNCLDAKACNLDDTCK 169
Db 120 CIPENYTKKCCANGYSRLP--GRCVVINECAEPRLNCGNAECIDLAEGY---TC-Q 173
QY 170 YRSAYITPCTTSMNSNEVCNR-----KCHKALRPF- 199
Db 174 CRSGYADISPVQPGRICRARNECNSKEKYVDCSENAICADTEHSYSCRCRPFADVS 233
QY 200 --PKVP-----AKHSYGMFLFCGR----- 217
Db 234 AAFKRLPGRCIEAVNECAPSLDCKNAFCEDKEG--ICRCRPGYVNSPNAARH 290
QY 218 -----DIACTERRRQTIIVPCSYEE-----RERFNC----- 243
Db 291 PGRICTRVEKIKTDKTSBSTDGCDBPN-----PRCGANEAQVQHGHCCEVETA 345
QY 244 -----LSLQDSCKTNYICRSLADFTNCPQ-----SRSV 274
Db 346 PRYTDGSCRYVSAKSKRNTCDKNAICLNRFDSYTCQCRPGYIDLADLTNAPGRICKELI 405
QY 275 SNCKLEN-----YADCLAYSGLIGTWTPNVYD--SSSLVAPKWCDCSNGDLDCLKF 328
Db 406 NECASSDNECSPPYACIDATNGYACQCL--DGFIDVSSRYNKPGRGQCTNSNECSE--KS 462
QY 329 LNFEDNTCLKNA-----IOAFNGSDVTVMQAPVPQTTATT 368
Db 463 L-----NTCDENADCVDTIPDGYTCQCYGPFVDVSSNANLPGRVCTVQTT 507

```

RESULT 3

A49128

cell-fate determining gene Notch2 protein - rat

C/Species: *Rattus norvegicus* (Norway rat)

C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C/Accession: A49128

R:Weinmaster, G.; Roberts, V.J.; Lemke, G.

Development 116, 931-941, 1992

A:Title: Notch2: a second mammalian Notch gene.

A/Reference number: A49128; MUID:93202015; PMID:1295745

A/Accession: A49128

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-2471 <WEI>

A/Cross-references: UNIPROT:Q9QW30

A:Experimental source: Schwann cell

C:Note: sequence extracted from NCBI backbone (NCBI:P:127811)

C/Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F:1264-235/Domain: EGF homology <EGF1>

F:799-830/Domain: EGF homology <EGF1>

F:877-908/Domain: EGF homology <EGF2>

F:1029-1060/Domain: EGF homology <EGF3>

F:1067-1098/Domain: EGF homology <EGF3>

F:1153-1184/Domain: EGF homology <EGF3>

F:1181-1222/Domain: EGF homology <EGF4>

F:1876-1908/Domain: ankyrin repeat homology <AN1>

F:1909-1941/Domain: ankyrin repeat homology <AN2>

F:1943-1975/Domain: ankyrin repeat homology <AN3>

F:1976-2008/Domain: ankyrin repeat homology <AN4>

F:2009-2041/Domain: ankyrin repeat homology <AN5>

Query Match 5.3%; Score 131; DB 2; Length 2471;
 Best Local Similarity 19.8%; Pred. No. 0.25;
 Matches 117; Conservative 63; Mismatches 195; Indels 216; Gaps 31;

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QY 23 GGDRLDVCYA-----SDCLKEGSCSTKRTLR-----QVAGKETNFSLTSGI 66
Db 1169 GGYRCECPGVGYVNCSEYEDC--QNPCCQNGTCTIDLNVHFKSCPPG-----TRGL 1220
QY 67 ---FAKDECRSAMBALKOKSL-----YNCRCKRMKEKNCIRIYMSWYQSLQGNLLE 117
Db 1221 LCEENIDDCAGAPICLNGGQCVDRIGYSCRLPFGAGER-----CEG----- 1263
QY 118 DSPYEPVNSRLSDIFRAVPFISDFQGVENHISKNNCLDAKACNLDDT--CKYRSAYI 175
Db 1264 -----DI-----NECL--SNPCSSSEGSIDCTQLKNYQ 1289
QY 176 TPCTTSMN-----EVCNRKC-----HKALRPFQVPAKHSYGMFLFCGRDI 219
Db 1290 CVCSAFLGRHCTETFLVCPQKPLNGTCVAVSNVPDGFICRCRPGFSGARCQSSCGOV 1349
QY 220 ACTERRRQTIIVPCSYEERERPNCLSLQDSCKT-----YICRSLADP 263
Db 1350 KC--RREGQCVHTASGHCPCFPNKHKDESGCASPCQHGTCYPRQRPPIYSGRCBPFFW 1407
QY 264 FTNCQ-----PERSVSNCLKENYADCLAYSGLIGTWTPNVY--DSSSLVAPKWC 314
Db 1408 GSHCESYATPSTPAPCTCLSGYCAD--KARDGICDEACNSHACQMDGDSLTMEDPMAN 1465
QY 315 CSNS-----GNLDE-----DCLKTLNF-----FDQNTCLK--NA 341
Db 1466 CTSILRCWEYINNOCDLCTAECT--PDNFCQNSYTKCYDKXCADHFDONHCDKGCNN 1524
QY 342 IOAFNGSDVTVMQAPVPQTTATT-----APPVQTTATT-----TAFRVNKKPL 378
Db 1525 EECGWDGLDCAADQPENLABGILYIVLLPPEQLDQSRFLAIGTLHTNIRIQDQ 1584
QY 379 G-----PAGSENEIPTHVLPCCANLQAKL--KSNVSGSTHCLSDSD--FG 421
Db 1585 GALMVFYFYGRKSAAMKKQVARRSLP--DEGQOIIIGSKVLEIDNRQCVDDQCFK 1641
QY 422 KDGLAGA--SSHITTKSMAAPSCSLG-----SLPILMTALAAALLSVL 464
Db 1642 NTDAAMALLASHAIOGTLSTPLVSVSESDPRTPLLYLAAVAVIILFL 1692

```

RESULT 4

S04847

leukocyte adhesion protein CD18 precursor - mouse

C/Species: *Mus musculus* (house mouse)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C/Accession: S04847

R:Wilson, R.W.; O'Brien, W.F.; Beaudet, A.L.

Nucleic Acids Res. 17, 5397, 1989

A:Title: Nucleotide sequence of the cDNA from the mouse leukocyte adhesion protein CD18.

A/Reference number: S04847; MUID:89345112; PMID:2569711

A/Accession: S04847

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:13 ; Search time 181 Seconds

(without alignments)
1324.050 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488
Sequence: 1 MPALATYFPLPLDLMSAE.....PVLMLTRALLLSVSLAETS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488	100.0	468	1	GPR1_RAT
2	2458	98.8	468	2	O35246
3	2452	98.6	468	1	GPR1_MOUSE
4	2449.5	98.5	463	2	O35748
5	2419.5	97.2	463	2	O35252
6	2316.5	93.1	465	1	GPR1_HUMAN
7	1914.5	76.9	469	1	GPR1_CHICK
8	1548.5	62.2	472	2	O98TT9
9	1453.5	58.4	481	2	O98TT8
10	1158	46.5	225	2	O9QWK2
11	1120.5	45.0	464	2	O35977
12	1112.5	44.7	463	1	GPR2_MOUSE
13	1110.5	44.6	463	2	O920V3
14	1109.5	44.6	464	1	GPR2_HUMAN
15	1098.5	44.2	444	2	O792X9
16	1076.5	43.3	465	1	GPR2_CHICK
17	984.5	39.6	431	1	GPR1_CHICK
18	974.5	39.2	458	2	O6T5C3
19	860	34.6	395	2	O922A3
20	792	31.8	331	2	O725E2
21	790	31.8	330	2	O922A2
22	513	20.6	109	2	O8JG58
23	511	20.5	400	1	GPR3_HUMAN
24	505.5	20.3	397	1	GPR3_MOUSE
25	505	20.3	385	2	O9R2D0
26	504	20.3	397	2	O6AXR3
27	462	18.6	273	1	GPR4_RAT
28	452	18.2	260	1	GPR4_MOUSE
29	388	15.6	299	1	GPR4_HUMAN
30	367.5	14.8	222	2	O9Q2G2
31	214	8.6	394	2	O6UXY0

32	204.5	8.2	393	2	O6SJ00	O6SJ00 mus musculu
33	194.5	7.8	77	2	O91I87	O91I87 ratu
34	168	6.8	238	2	O6SJD9	O6SJD9 mus musculu
35	154.5	6.2	502	2	O7QDB4	O7QDB4 anopheles g
36	150	6.0	3183	2	O6SZC2	O6SZC2 caenorhabdi
37	150	6.0	3767	1	MUA3 CAEEL	P34576 caenorhabdi
38	135.5	5.4	814	2	O7RIV1	O7RIV1 giardia lam
39	134.5	5.4	2585	2	O23587	O23587 caenorhabdi
40	131	5.3	2471	1	NTC2_RAT	O9QW30 ratu
41	130.5	5.2	1289	2	O75JU6	O75JU6 dictyoste
42	129.5	5.2	1101	2	O964D2	O964D2 entamoeba h
43	129.5	5.2	1219	2	O95XG5	O95XG5 caenorhabdi
44	129	5.2	771	1	ITB2_MOUSE	P11835 mus musculu
45	129	5.2	2703	1	NOTC_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1
GPR1_RAT STANDARD; PRT; 468 AA.
ID GPR1_RAT
AC O62997;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE GDNF family receptor alpha 1 precursor (GPR-alpha 1) (GDNF receptor 1) (GPR1)
DE alpha (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor 1) (RET ligand 1)
GN Name=Gfral; Synonyms=Gdnfra, Retl1, Trnr1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96270513; PubMed=8674117; DOI=10.1016/S0092-8674(00)81311-2;
RA Jing S., Wen D., Yu Y., Holst P.L., Luo Y., Fang M., Tamir R.,
RA Antonio L., Hu Z., Cupples R., Louis J.-C., Hu S., Altrock B.W.,
RA Fox G.M.;
RT "GDNF-induced activation of the ret protein tyrosine kinase is mediated by GDNFR-alpha, a novel receptor for GDNF.";
RT Cell 85:1113-1124(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistral; TISSUE=Kidney;
RX MEDLINE=97323236; PubMed=9177201; DOI=10.1073/pnas.94.12.6238;
RA Sanicola M., Hession C.A., Worley D.S., Carmilio P., Ehrenfeld C.,
RA Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitley A.,
RA Papinsky R.B., Cate R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96273032; PubMed=8657309; DOI=10.1038/382080a0;
RA Treanor J.T.S., Goodman L., de Sauvage F., Stone D.M., Poulsen K.T.,
RA Beck C.D., Gray C., Aymann L.P., Pollock R.A., Hefti F.,
RA Phillips H.S., Goddard A., Moore M.W., Bui-Bello A., Davies A.M.,
RA Arai N., Takahashi M., Vanden R., Henderson C.E., Rosenthal A.;
RT "Characterization of a multicomponent receptor for GDNF.";
RT Nature 382:80-83(1996).
RL -1- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced autophosphorylation and activation of the RET receptor.
CC -1- SUBUNIT: 2 molecules of GDNFR-alpha are thought to form a complex with the disulfide-linked GDNF dimer and with 2 molecules of RET.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Expressed in liver, brain and kidney.
CC -1- SIMILARITY: Belongs to the GDNFR family.
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CC -----
 DR EMBL; U59486; AAC52663.1; -
 DR EMBL; U97142; AAC53300.1; -
 DR RGD; 2681; Gfrel.
 DR InterPro; IPR003438; GDNF_Receptor.
 DR Pfam; PF02351; GDNF.1.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Glycoprotein; Gpi-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 430 GDNF family receptor alpha 1.
 FT PROPEP 431 468 Removed in mature form (Potential).
 FT DOMAIN 362 369 Poly-Thr.
 FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 406 406 N-linked (GlcNAc...) (Potential).
 FT LIPID 430 430 GPI-anchor amidated serine (Potential).
 SQ SEQUENCE 468 AA: 51649 MW: 8285906502580F CRC64;

Query Match 100.0%; Score 2488; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 2.5e-179;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLLATLYPALPLDLLMSAEVSGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 DB 1 MFLLATLYPALPLDLLMSAEVSGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRGMKEKNCRLRYMSYQSLQGNLLEDSF 120
 DB 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRGMKEKNCRLRYMSYQSLQGNLLEDSF 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRCKCHALRQFPDKVPKSHYGMFSCSDIACHTERRRQTIIVPCSYEERER 240
 DB 181 SMSNEVCNRCKCHALRQFPDKVPKSHYGMFSCSDIACHTERRRQTIIVPCSYEERER 240
 QY 241 PNCISLQDSCKTNYICRSLADFTNCPESRSVNCLEKADCLAYSGIIGVMTFN 300
 DB 241 PNCISLQDSCKTNYICRSLADFTNCPESRSVNCLEKADCLAYSGIIGVMTFN 300
 QY 301 YVDSSSLSVAPWDCSNGNDLEDCLKPLNPKDNTCLKNALQAFNGSDVTMMQAPPV 360
 DB 301 YVDSSSLSVAPWDCSNGNDLEDCLKPLNPKDNTCLKNALQAFNGSDVTMMQAPPV 360
 QY 361 OTTATATTTAFVKNKPLGPAGSENEIPHVLPCANIQAOQLCKSNVSGSTHCLSDSPF 420
 DB 361 OTTATATTTAFVKNKPLGPAGSENEIPHVLPCANIQAOQLCKSNVSGSTHCLSDSPF 420
 QY 421 GKDLGAGASHITTKSMAPPSCSLSPLVLMTLAALLSYLAETS 468
 DB 421 GKDLGAGASHITTKSMAPPSCSLSPLVLMTLAALLSYLAETS 468

RESULT 2
 ID 035246 PRELIMINARY; PRT: 468 AA.
 AC 035246;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE GDNF receptor alpha (Glial cell line derived neurotrophic factor family receptor alpha 1).
 GN Name=Gfrel; Synonyms=GDNF-alpha;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57; TISSUE=Liver;
 RX MEDLINE=96252741; PubMed=9592044;
 RA Dey B.K., Wong Y.W., Too H.P.;
 RT "Cloning of a novel murine isoform of the glial cell line-derived neurotrophic factor receptor";
 RL Neuroreport 9:37-42(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
 RA Brownstein M.J., Usdin T.B., Toshlyuk S., Carninci P., Mullany S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravitski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014117; AAB86599.1; -
 DR EMBL; BC054378; AAB84378.1; -
 DR MGI; MGI:1100842; Gfrel.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0019898; C:extrinsic to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0009653; P:morphogenesis; TAS.
 DR GO; GO:0007399; P:neurogenesis; IMP.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
 DR InterPro; IPR003438; GDNF_Receptor.
 DR InterPro; IPR003503; GDNF_Receptor1.
 DR Pfam; PF02351; GDNF.1.
 DR PRINTS; PR01317; GDNFRALPHA1.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW RECEPTOR.
 SQ SEQUENCE 468 AA: 51751 MW: 997105C2A6DD6446 CRC64;
 Query Match 98.8%; Score 2458; DB 2; Length 468;
 Best Local Similarity 97.6%; Pred. No. 4.7e-177;
 Matches 457; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFLLATLYPALPLDLLMSAEVSGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 DB 1 MFLLATLYPALPLDLLMSAEVSGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRGMKEKNCRLRYMSYQSLQGNLLEDSF 120
 DB 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRGMKEKNCRLRYMSYQSLQGNLLEDSF 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRCKCHALRQFPDKVPKSHYGMFSCSDIACHTERRRQTIIVPCSYEERER 240
 DB 181 SMSNEVCNRCKCHALRQFPDKVPKSHYGMFSCSDIACHTERRRQTIIVPCSYEERER 240

Db 181. SMSNEVCNRRKCHKALRQFFDKVPAAKHSYGMLFCSGRDVACTERRRQTIIVPVCSYEERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLI GTWTPN 300
 Db 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLI GTWTPN 300
 QY 301 YVDSSLSVAWPCDCNSGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTMMQAPAPV 360
 Db 301 YVDSSLSVAWPCDCNSGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTMMQAPAPV 360
 QY 361 QTTATTTTAFRYKRNKPLGAGSENEIPTHVLPCCANIQAOKLSNVSGSTHCLSDSDP 420
 Db 361 QTTATTTTAFRYKRNKPLGAGSENEIPTHVLPCCANIQAOKLSNVSGSTHCLSDSDP 420
 QY 421 GKQGLAGASSHITTKSMAAPPSGSLSPVLMLTALALISVLAETS 468
 Db 421 GKQGLAGASSHITTKSMAAPPSGSLSPVLMLTALALISVLAETS 468

RESULT 3

GFR1_MOUSE STANDARD; PRT; 468 AA.

ID GFR1_MOUSE
 AC P97785;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 44, Last annotation update)
 DE GDNF family receptor (GFR-alpha 1) (GDNF receptor alpha) (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor 1).
 DE Name=Gfral; Synonyms=Gdnfra, Trnrl;
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NCB1
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dorsal root ganglion;
 RA Matabe K.; (Feb-1997) to the EMBL/GenBank/DBJ databases.
 CC Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced autophosphorylation and activation of the RET receptor (By similarity).
 CC -1- SUBUNIT: 2 molecules of GDNFR-alpha are thought to form a complex with the disulfide-linked GDNF dimer and with 2 molecules of RET (By similarity).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -1- SIMILARITY: Belongs to the GDNFR family.
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CC EMBL; AB008080; BAA19185.1; -
 CC MGD; MG11100842; Gfral.
 CC InterPro: IPR003438; GDNF_receptor.
 CC Pfam: PF02351; GDNF; 1.
 CC PRINTS; PR01316; GDNFRRECEPTOR.
 CC SIGNAL
 CC 1
 CC 24
 CC 25 430 GDNF family receptor alpha 1.
 CC 26 468 GDNF in mature form (Potential).
 CC 27 468 Thr-rich.
 CC 28 369 N-linked (GlcNAc. . .) (Potential).
 CC 29 359 N-linked (GlcNAc. . .) (Potential).
 CC 30 347 N-linked (GlcNAc. . .) (Potential).
 CC 31 406 N-linked (GlcNAc. . .) (Potential).
 CC 32 430 GPI-anchor amidated serine (Potential).
 CC 33 468 AA; 51782 MW; AAB393177307212 CRC64;

Query Match 98.6%; Score 2452; DB 1; Length 468;
 Best Local Similarity 97.4%; Pred. No. 1.3e-176;
 Matches 456; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFATATYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 Db 1 MFATATYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 QY 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKERKCLRIYWSYQSLQGNLLEDSP 120
 Db 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKERKCLRIYWSYQSLQGNLLEDSP 120
 QY 121 YEVNRLSDIFRAVFIIDVPOOVHISGNNCLDAARCNLDPTCKKRSAYITPCTT 180
 Db 121 YEVNRLSDIFRAVFIIDVPOOVHISGNNCLDAARCNLDPTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRKCHKALRQFFDKVPAAKHSYGMLFCSGRDVACTERRRQTIIVPVCSYEERER 240
 Db 181 SMSNEVCNRRKCHKALRQFFDKVPAAKHSYGMLFCSGRDVACTERRRQTIIVPVCSYEERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLI GTWTPN 300
 Db 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLI GTWTPN 300
 QY 301 YVDSSLSVAWPCDCNSGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTMMQAPAPV 360
 Db 301 YVDSSLSVAWPCDCNSGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTMMQAPAPV 360
 QY 361 QTTATTTTAFRYKRNKPLGAGSENEIPTHVLPCCANIQAOKLSNVSGSTHCLSDSDP 420
 Db 361 QTTATTTTAFRYKRNKPLGAGSENEIPTHVLPCCANIQAOKLSNVSGSTHCLSDSDP 420
 QY 421 GKQGLAGASSHITTKSMAAPPSGSLSPVLMLTALALISVLAETS 468
 Db 421 GKQGLAGASSHITTKSMAAPPSGSLSPVLMLTALALISVLAETS 468

RESULT 4

ID 035748 PRELIMINARY; PRT; 463 AA.

AC 035748;
 DT 01-JAN-1998 (T-EMBLrel. 05, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DE GDNFR-alpha/Trnrl-delta protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN NCB1
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hannover;
 RA Zhong J.; Annies M.; Heumann R.;
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 CC EMBL; A002072; CAA05171.1; -
 CC PIR; S69080; S69080.
 CC GO; GO:0004872; F:receptor activity; IEA.
 CC InterPro: IPR003438; GDNF_receptor.
 CC Pfam: PF02351; GDNF; 1.
 CC PRINTS; PR01317; GDNFRALPHA1.
 CC PRINTS; PR01316; GDNFRRECEPTOR.
 CC SIGNAL
 CC 463 AA; 51032 MW; CCC9583ACE7353CA CRC64;

Query Match 98.5%; Score 2449.5; DB 2; Length 463;
 Best Local Similarity 98.9%; Pred. No. 2e-176; 0; Indels 5; Gaps 1;
 Matches 463; Conservative 0; Mismatches 0;

QY 1 MFATATYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 Db 1 MFATATYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 QY 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKERKCLRIYWSYQSLQGNLLEDSP 120
 Db 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKERKCLRIYWSYQSLQGNLLEDSP 120

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Db 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGKKEKNCRLIYWSMYQSLQGNLDLEDSP 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
Db 121 YEPVNSRLSDIFRAVPFIS-----VEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 175
QY 181 SMSNEVCNRRCKHARLQFDPKVPAPKSYGMFLFSCGRDIACCTERRRQTIIVPCSYEBER 240
Db 176 SMSNEVCNRRCKHARLQFDPKVPAPKSYGMFLFSCGRDIACCTERRRQTIIVPCSYEBER 235
QY 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGTWTPTN 300
Db 236 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGTWTPTN 295
QY 301 YVDSLSLVAPWCSCNSGNDLEDCLKFLNFKDNTCLKNAIOAFNGSDVTWMPAPPV 360
Db 296 YVDSLSLVAPWCSCNSGNDLEDCLKFLNFKDNTCLKNAIOAFNGSDVTWMPAPPV 355
QY 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPFCANLQAOGLKSNVSGSTHCLSDSP 420
Db 356 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPFCANLQAOGLKSNVSGSTHCLSDSP 415
QY 421 GKDGLAGASHITTKSMAPPSCLSSLPVLMLTALAALLSVSLAETS 468
Db 416 GKDGLAGASHITTKSMAPPSCLSSLPVLMLTALAALLSVSLAETS 463

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RESULT 5

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035252 PRELIMINARY; PRT; 463 AA.
ID 035252;
AC 035252;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE GDNF receptor beta.
GN Name=Gfrial; Synonyms=GDNFR-beta;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57;
RX MEDLINE=98252741; PubMed=9592044;
RA Dey B.K., Wong Y.W., Too H.P.;
RT "Cloning of a novel murine isoform of the glial cell line-derived
RT neurotrophic factor receptor."
RL Neuroreport 9:37-42(1998).
DR EMBL; AF015172; AAB86600.1; -.
DR MGD; MGI:1100842; Gfrial.
DR GO; GO:0005615; Cytoplasmic space; TAS.
DR GO; GO:0019898; Cytoplasmic to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR GO; GO:0007399; P:neurogenesis; IMP.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003503; GDNF_receptor.
DR Pfam; PF02351; GDNFR1.
DR PRINTS; PRO1317; GDNFR1ALPHA.
DR PRINTS; PRO1316; GDNFR1ALPHA.
KM RECEPTOR.
SQ SEQUENCE 463 AA; 51134 MW; EAF2A1522622C037 CRC64;

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Query Match 97.2%; Score 2419.5; DB 2; Length 463;
 Best Local Similarity 96.6%; Pred. No. 3.7e-174;
 Matches 452; Conservative 8; Mismatches 3; Indels 5; Gaps 1;

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QY 1 MFATLTYFALPLDLILMSAVSAGGRLLDVCVADCKLEQSGSTKYRTLRQVAKETNPF 60
Db 1 MFATLTYFVPLDLILMSAVSAGGRLLDVCVADCKLEQSGSTKYRTLRQVAKETNPF 60

```

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QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGKKEKNCRLIYWSMYQSLQGNLDLEDSP 120
Db 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGKKEKNCRLIYWSMYQSLQGNLDLEDSP 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
Db 121 YEPVNSRLSDIFRAVPFIS-----VEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 175
QY 181 SMSNEVCNRRCKHARLQFDPKVPAPKSYGMFLFSCGRDIACCTERRRQTIIVPCSYEBER 240
Db 176 SMSNEVCNRRCKHARLQFDPKVPAPKSYGMFLFSCGRDIACCTERRRQTIIVPCSYEBER 235
QY 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGTWTPTN 300
Db 236 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGTWTPTN 295
QY 301 YVDSLSLVAPWCSCNSGNDLEDCLKFLNFKDNTCLKNAIOAFNGSDVTWMPAPPV 360
Db 296 YVDSLSLVAPWCSCNSGNDLEDCLKFLNFKDNTCLKNAIOAFNGSDVTWMPAPPV 355
QY 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPFCANLQAOGLKSNVSGSTHCLSDSP 420
Db 356 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPFCANLQAOGLKSNVSGSTHCLSDNDY 415
QY 421 GKDGLAGASHITTKSMAPPSCLSSLPVLMLTALAALLSVSLAETS 468
Db 416 GKDGLAGASHITTKSMAPPSCLSSLPVLMLTALAALLSVSLAETS 463

```

RESULT 6

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ID GFR1_HUMAN STANDARD; PRT; 465 AA.
AC P56159; O15507; O43912;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE GDNF family receptor alpha 1 precursor (GFR-alpha 1) (GDNF receptor
DE alpha) (GDNFR-alpha) (GFR-beta related neurotrophic factor receptor 1)
DE (Ref.1)
GN Name=GFRAL1; Synonyms=GDNFRA, RETL1, TRNR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Substantia nigra;
RX MEDLINE=96270513; PubMed=8674117; DOI=10.1016/S0092-8674(00)81311-2;
RA Jing S., Wen D., Yu Y., Holst P.L., Luo Y., Fang M., Tamil R.,
RA Antonio L., Hu Z., Cupples R., Louis J.-C., Hu S., Altrock B.W.,
RA Fox G.M.;
RT "GDNF-induced activation of the ret protein tyrosine kinase is
RT mediated by GDNFR-alpha, a novel receptor for GDNF."
RL Cell 85:1113-1124(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney;
RX MEDLINE=97322356; PubMed=9177201; DOI=10.1073/pnas.94.12.6238;
RA Santicola M., Hesbion C.A., Worley D.S., Camillo P., Ehrenfels C.,
RA Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitty A.,
RA Pepinsky R.B., Cate R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
RT can be mediated by two different cell-surface accessory proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS ASN-85 AND ALA-366.
RX MEDLINE=98207251; PubMed=9545641; DOI=10.1006/geno.1997.5191;
RA Angrier M., Jing S., Bolk S., Bentley K., Nallaamy S., Hatushka M.,
RA Fox G.M., Chakravarti A.;
RT "Human GFRAL1: cloning, mapping, genomic structure, and evaluation as a
RT candidate gene for Hirschprung disease susceptibility."
RL Genomics 48:354-362(1998).
RN [4]

```


RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thyroid carcinoma;
RX MEDLINE=9820874; PubMed=9600247;
RA Shetliffe S.E., Khorana S., Schultze P.N., Huang E., Thobe N.,
Hu Z.J., Fox G.M., Jing S., Cote G.J., Gargel R.F.;
RT "Molecular analysis of the GDNF/RET-GDNF-alpha signaling complex in
a kindred with vesicoureteral reflux.";
RL Hum. Genet. 102:474-478(1998).
RN (5)
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Substantia nigra;
RA Hishiki T., Kondoh K., Ichimiya S., Mimura Y., Seki N., Ozaki T.,
Sakiyama S., Takahashi H., Ohnuma N., Tanabe M., Fujimura S.,
Nakagawa A.;
RT "GDNF-induced differentiation and its enhancement by retinoic acid in
primary human neuroblastomas expressing c-Ret and GDNF-alpha.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko U., Marziani K., Farmer A.A., Rubin G.M., Hong J.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Browstein M.J., Ustin T.B., Tothiyuki S., Abramson R.D., Mullahy S.J.,
Bosak S.A., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (7)
RP SPLICED ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=1475258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
RN (8)
RP VARIANTS ALA-366 AND ARG-371.
RX PubMed=1456559; DOI=10.1007/s00439-003-1036-z;
RA Sasaki A., Kanai M., Kijima K., Akaba K., Hashimoto M., Hasegawa H.,
Otsaki S., Koizumi T., Kusuda S., Ogawa Y., Tuchiya K., Yamamoto W.,
Nakamura T., Hayasaka K.;
RT "Molecular analysis of congenital central hypoventilation syndrome.";
RL Hum. Genet. 114:22-26(2003).
CC -1- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced
autophosphorylation and activation of the RET receptor (By
similarity).
CC -1- SUBUNIT: 2 molecules of GDNF-alpha are thought to form a complex
with the disulfide-linked GDNF dimer and with 2 molecules of RET
(By similarity).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P56159-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P56159-2; Sequence=VSP_001660;
CC Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC -1- SIMILARITY: Belongs to the GDNF family.

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CC
CC EMBL; U97144; AAC51646.1; -;
CC EMBL; AF038420; AAC39693.1; -;
CC EMBL; AF038411; AAC39693.1; JOINED.
CC EMBL; AF038412; AAC39693.1; JOINED.
CC EMBL; AF038413; AAC39693.1; JOINED.
CC EMBL; AF038414; AAC39693.1; JOINED.
CC EMBL; AF038415; AAC39693.1; JOINED.
CC EMBL; AF038416; AAC39693.1; JOINED.
CC EMBL; AF038417; AAC39693.1; JOINED.
CC EMBL; AF038418; AAC39693.1; JOINED.
CC EMBL; AF038419; AAC39693.1; JOINED.
CC EMBL; AF038421; AAC39692.1; -;
CC EMBL; AF042080; AAB97371.1; -;
CC EMBL; AF058990; AAC14431.1; -;
CC EMBL; AF058991; AAC14431.1; JOINED.
CC EMBL; AF058992; AAC14431.1; JOINED.
CC EMBL; AF058993; AAC14431.1; JOINED.
CC EMBL; AF058994; AAC14431.1; JOINED.
CC EMBL; AF058995; AAC14431.1; JOINED.
CC EMBL; AF058996; AAC14431.1; JOINED.
CC EMBL; AF058997; AAC14431.1; JOINED.
CC EMBL; AF058998; AAC14431.1; JOINED.
CC EMBL; U95847; AAB71811.1; -;
CC EMBL; BC014962; AAB14962.1; -;
CC H-InvDB; HIX0009233; -;
CC DR MM; 601496; -;
CC DR GO; GO:0019898; C:extrinsic to membrane; NAS.
CC DR GO; GO:0004872; F:receptor activity; NAS.
CC DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NAS.
CC DR InterPro; IPR003438; GDNF_receptor.
CC DR Pfam; PF02351; GDNF_1.
CC DR PRINTS; PR01316; GDNFRECEPTOR.
CC KW Alternative splicing; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
CC FT Polymorphism; Receptor; Signal.
CC FT SIGNAL 1 24 Potential.
CC FT CHAIN 25 429 GDNF family receptor alpha 1.
CC FT PROPEP 430 465 Removed in mature form (Potential).
CC FT DOMAIN 362 369 Poly-Thr.
CC FT CARBOHYD 359 359 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 406 406 N-linked (GlcNAc...) (Potential).
CC FT LIPID 429 429 GPI-anchor amidated serine (Potential).
CC FT VARSPPLIC 140 144 Missing (in isoform 2).
CC FT VARIANT 85 85 Y -> N (in dbSNP:8192662).
CC FT VARIANT 366 366 /FTG=VAR_012488.
CC FT VARIANT 371 371 T -> A (in dbSNP:2072276).
CC FT VARIANT 371 371 L -> R (may be involved in congenital
central hypoventilation syndrome).
CC FT CONFLICT 245 245 /FTId=VAR_018261.
CC FT CONFLICT 358 358 Missing (in Ref. 1).
CC FT SEQUENCE 465 AA; 51455 MW; 91A550D06A6777BD CRC64;
CC
CC Query Match 93.1%; Score 2316.5; DB 1; Length 465;
CC Best Local Similarity 92.7%; Pred. No. 2.2e-166;
CC Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;
CC
CC QY 1 MFATATYFALPLDLILMSAVSGDRLDCVKASDQCLKQSGCTKYRTLRQCVAGKRTNF 60
CC DB 1 MFATATYFALPLDLILMSAVSGDRLDCVKASDQCLKQSGCTKYRTLRQCVAGKRTNF 60

```

QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKCKNCLRIYMSYOSLGNDLLEBSP 120
DB 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKCKNCLRIYMSYOSLGNDLLEBSP 120
QY 121 YEPNRSRLSDIFRAVPFISDVFOQVEHISKGNKCLDAKACMLDTCCKYRSAYITPCTT 180
DB 121 YEPNRSRLSDIFRAVPFISDVFOQVEHISKGNKCLDAKACMLDTCCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFPDVKPAKSYGMFLFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SVSNDVCNRKCHKALROFPDVKPAKSYGMFLFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCISLSDSCCTNYICRSRLADFTNQCPSRSVSNCKENYADCLLAYSGLIGTWMTPN 300
DB 241 PNCISLSDSCCTNYICRSRLADFTNQCPSRSVSNCKENYADCLLAYSGLIGTWMTPN 300
QY 301 YVDSSSSVAPWCCNSGNDLECLKPLNFKDNTCLKNAIQARNGSDYTMQPAFV 360
DB 301 YVDSSSSVAPWCCNSGNDLECLKPLNFKDNTCLKNAIQARNGSDYTMQPAFV 360
QY 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSGTHLCLSDPF 420
DB 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSGTHLCLSDPF 420
QY 421 GKDLGAGASHITTKSMAAPSGSLSLPVLMTLALSLVSLAETS 468
DB 421 EKELGAGASHITTKSMAAPSGSLSLPVLMTLALSLVSLAETS 468

```

RESULT 7

GFRL_CHICK STANDARD; PRT; 469 AA.

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AC 013156;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE GDNF family receptor alpha 1 precursor (GFR-alpha 1) (GDNF receptor
DE alpha) (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor
DE 1).
GN Name=GFRAL1; Synonyms=GDNFRA1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97336104; PubMed=9192899; DOI=10.1038/42729;
RA Buf-Bello A., Adu J., Pinon L.G.P., Horton A., Thompson J.,
RA Rosenthal A., Chinchetru M., Buchman V.L., Davies A.M.;
RT "Neurturin responsiveness requires a GPI-linked receptor and the Ret
RT receptor tyrosine kinase.";
RL Nature 387:721-724(1997).
CC -!- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced
CC autophosphorylation and activation of the RET receptor (By
CC similarity).
CC -!- SUBUNIT: 2 molecules of GDNFR-alpha are thought to form a complex
CC with the disulfide-linked GDNF dimer and with 2 molecules of RET
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: Belongs to the GDNFR family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
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CC EMBL; U90541; AAB61570.1; -.

```

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DR InterPro; IPR003438; GDNF_receptor.
DR Pfam; PF02351; GDNF.1.
DR PRINTS; PR01316; GDNFRRECEPTOR.
KW Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 430 GDNF family receptor alpha 1.
FT PROPEP 431 469 Removed in mature form (Potential).
FT DOMAIN 361 368 Poly-Thr.
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 346 346 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 405 405 N-linked (GlcNAc...) (Potential).
FT LIPID 430 430 GPI-anchor amidated serine (Potential).
SQ SEQUENCE 469 AA; 52043 MW; B9DB8ED15218AF39 CRC64;

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Query Match 76.9%; Score 1914.5; DB 1; Length 469;
 Best Local Similarity 77.7%; Pred. No. 4.6e-136;
 Matches 366; Conservative 42; Mismatches 48; Indels 15; Gaps 8;

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QY 1 MELATYALPLDLILMSAEVS---GGRLDVCVASDQCLKEQSCSTKRYTLRQCVAGKE 57
DB 1 MELATYALPLDLILMSAEVSGLPGGRDLDCVARSQCLKEQSCSTKRYTLRQCVAGKE 60
QY 58 TNFSITSGLEAKDECRSAMEALKOKSLYNCRCKRGMKCKNCLRIYMSYOSLGNDLLE 117
DB 61 SNFSRATGLKAEKDECKSAMEALKOKSLYNCRCKRGMKCKNCLRIYMSYOSLGNDLLE 120
QY 118 DSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNKCLDAKACMLDTCCKYRSAYIT 176
DB 121 DSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNKCLDAKACMLDTCCKYRSAYIT 175
QY 177 PCTTSMNEVCNRKCHKALROFPDVKPAKSYGMFLFCSCRDIACTERRRQTIIVPCSYE 236
DB 176 PCTTSMNEVCNRKCHKALROFPDVKPAKSYGMFLFCSCRDIACTERRRQTIIVPCSYE 235
QY 237 EBERNCISLSDSCCTNYICRSRLADFTNQCPSRSVSNCKENYADCLLAYSGLIGTV 296
DB 236 EBERNCISLSDSCCTNYICRSRLADFTNQCPSRSVSNCKENYADCLLAYSGLIGTV 295
QY 297 MTPNVDSSSVAPWCCNSGNDLECLKPLNFKDNTCLKNAIQARNGSDYTMQPAFV 356
DB 296 MTPNVDSSSVAPWCCNSGNDLECLKPLNFKDNTCLKNAIQARNGSDYTMQPAFV 355
QY 357 APVQTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSGTHLCLSDPF 414
DB 356 ILPVQTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSGTHLCLSDPF 413
QY 415 LSDSPFGDGLAGAS-SHITTKSMAAPSGSLSLPVLMTLALSLVSLAETS 463
DB 414 LNEAIGDNDTPGVSTSHISENSFALPTSPFPTPLMTLALSLFLPLS 464

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RESULT 8

Q98TT9 PRELIMINARY; PRT; 472 AA.

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AC 098TT9;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE GDNF family receptor alpha-1a.
GN Name=gfr1a; Synonyms=gfr1alpha1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RP SEQUENCE FROM N.A.
RX MEDLINE=21135398; PubMed=11237470; DOI=10.1006/dbio.2000.0145;
RA Shepherd I.T., Beattie C.E., Ratble D.W.;
RT "Functional analysis of zebrafish GDNF.";
RL Dev. Biol. 231:420-435(2001).

```

SEQUENCE FROM N.A.
 RX PubMed=14660438;
 RA Shepherd I.T., Pletsch J., Elworthy S., Kelsh R.N., Raible D.W.;
 RT "Roles for GFR(alpha)1 receptors in zebrafish enteric nervous system
 development.";
 RL Development 131:241-249(2004).
 DR EMBL: AY36320; AAK1260.2; -.
 DR ZFIN: ZDB-GENE-010226-2; gfr1a.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003438; GDNF_receptor.
 DR pfam: PF02351; GDNF_1.
 DR PRINTS: PR01317; GDNFPRALPAL.
 DR PRINTS: PR01316; GDNFRECEPTOR.
 KM RECEPTOR.
 SQ SEQUENCE 472 AA; 52742 MW; 7B5B0C436B299C7D CRC64;
 Query Match 62.2%; Score 1548.5; DB 2; Length 472;
 Best Local Similarity 62.2%; Pred. No. 1.9e-108;
 Matches 298; Conservative 60; Mismatches 90; Indels 31; Gaps 8;
 QY 1 MFATATYFALPLDLMLSAE---VSGDRLDVCVASDQCKEOSTKRTLRQCVAKE 57
 DB 1 MFATATYFALPLDLMLSAE---VSGDRLDVCVASDQCKEOSTKRTLRQCVAKE 60
 QY 58 TNSLTSLGSLAKDECRSAMEALKOKSLYNCRCKRGMKEKXCLRIYMSYOSLQNDL 117
 DB 61 SNFSMAGTAKDECRSLVDALQSPLYNCRCKRGMKEKXCLRIYMSYOSLQNDL 120
 QY 118 DSEYEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKKRSAYITP 177
 DB 121 DSEYEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKKRSAYITP 176
 QY 178 CTTSMNS-ENVNRRCKHAKALQPFDPKVPKASYSGLMFCSC---RDIACTERRRQITVPVC 233
 DB 177 CTSRVSSTAECNKRCKHAKALQPFDPKVPKASYSGLMFCSC---RDIACTERRRQITVPVC 236
 QY 234 SYEERERPNCLSLDSCCTNYTCRSRLADFTNCPQRSRSVSNCKENYADCLLAYSGL 233
 DB 237 SYEDKERPNCLTLQVSCCTNYTCRSRLADFTNCPQRSRSVSNCKENYADCLLAYSGL 236
 QY 294 GVTMTPNYVDSLSVAWPCDCSNGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTM 353
 DB 297 GVTMTPNYVDSLSVAWPCDCSNGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTM 356
 QY 354 WQAPAPVQTTATTTAATTAFFVKNKPLGPAAGSENEIPTHVLP-----CANLQAOQLKS 405
 DB 357 WHPMPVQTTTSMTPBQARADKDRSPNALIEPATIHNLNLPADNSLYQFCGNIQAQKKKT 416
 QY 406 NVGSGTHLCLSDDFGKDLGAGASHHTTSMAPPSCSLSLPVLMTLAALLSYSL 464
 DB 417 NNTIDV-LCVDPO-----IDPSSSNVTISKNSSPROMTISGLSGLL-----LLATSL 463
 RESULT 9
 Q98TT8 PRELIMINARY; PRT; 481 AA.
 AC Q98TT8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GDNF family receptor alpha-1b.
 GN Name=gfr1b; Synonyms=gfr1a1b;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21153398; PubMed=11237470; DOI=10.1006/dbio.2000.0145;
 RA Shepherd I.T., Beattie C.E., Raible D.W.;
 RT "Functional analysis of zebrafish GDNF.";

Dev. Biol. 231:420-435(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=14660438;
 RA Shepherd I.T., Pletsch J., Elworthy S., Kelsh R.N., Raible D.W.;
 RT "Roles for GFR(alpha)1 receptors in zebrafish enteric nervous system
 development.";
 RL Development 131:241-249(2004).
 DR EMBL: AY36321; AAK1261.2; -.
 DR ZFIN: ZDB-GENE-010226-3; gfr1b.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003438; GDNF_receptor.
 DR pfam: PF02351; GDNF_1.
 DR PRINTS: PR01316; GDNFRECEPTOR.
 KM RECEPTOR.
 SQ SEQUENCE 481 AA; 53639 MW; 478917653049CE23 CRC64;
 Query Match 58.4%; Score 1453.5; DB 2; Length 481;
 Best Local Similarity 59.8%; Pred. No. 2.8e-101;
 Matches 289; Conservative 56; Mismatches 95; Indels 43; Gaps 11;
 QY 1 MFATATYFALPLDLMLSAE---SGDRLDVCVASDQCKEOSTKRTLRQCVAKE 55
 DB 8 MFATATYFALPLDLMLSAE---SGDRLDVCVASDQCKEOSTKRTLRQCVAKE 67
 QY 56 KETNSLTSLGSLAKDECRSAMEALKOKSLYNCRCKRGMKEKXCLRIYMSYOSLQNDL 115
 DB 68 RTNPFMKKEPPEADQECRNALIBSMKOSPLYDCKCRGMKEKXCLRIYMSYOSLQNDL 127
 QY 116 LEDSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKKRSAYITP 175
 DB 128 LEDSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKKRSAYITP 183
 QY 176 TPCTTSMNS-NEVCNRRCKHAKALQPFDPKVPKASYSGLMFCSC---IACTEERRRQITVP 231
 DB 184 SPCTSVSTAEVCNKRCKHAKALQPFDPKVPKASYSGLMFCSC---IACTEERRRQITVP 243
 QY 232 VCSYERERPNCLSLDSCCTNYTCRSRLADFTNCPQRSRSVSNCKENYADCLLAYSGL 291
 DB 244 ACSYEDKERPNCLTLQVSCCTNYTCRSRLADFTNCPQRSRSVSNCKENYADCLLAYSGL 303
 QY 292 LGTWTTPNYVDSLSVAWPCDCSNGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTM 351
 DB 304 LGTWTTPNYVDSLSVAWPCDCSNGNDLEDCLKFLNPFKONTCLKNAIOAFNGSDVTM 363
 QY 352 TWMQAPAPVQTTATTTAATTAFFVKNKPLGPAAGSENEI-PTHVLP-----HVLPPCANLQ 399
 DB 364 GWQAPAPVQTTATTTAATTAFFVKNKPLGPAAGSENEI-PTHVLP-----HVLPPCANLQ 417
 QY 400 AOKLKSNGVSGTHLCLSDDFGKDLGAGASH-ITTKSMAPPSCSLSLPVLMTLAALLSYSL 457
 DB 418 AOKLKSNGVSGTHLCLSDDFGKDLGAGASH-ITTKSMAPPSCSLSLPVLMTLAALLSYSL 467
 QY 458 ALL 460
 DB 468 STL 470
 RESULT 10
 Q9QWK2 PRELIMINARY; PRT; 225 AA.
 AC Q9QWK2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GDNF receptor alpha (Fragment).
 GN Name=gfr1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

DR	InterPro; IPRO03504; GDNF_receptorA2.
DR	Pfam; PF02351; GDNF.1
DR	PRINTS; PR01318; GDNFRALPHA2.
DR	PRINTS; PR01316; GDNFRECEPTOR.
KW	Receptor.
SQ	SEQUENCE 464 AA; 51668 MW; 81168301BE50D6CC CRC64;
Query March	45.0%; Score 1120.5; DB 2; Length 464;
Best Local Similarity	47.6%; Pred. No. 3.5e-76;
Matches 224; Conservative	81; Mismatches 139; Indels 27; Gaps 9;
OY	1 MFAT---LYPAL--PLDLLMSAEVSGD-----RLDCVKASDOCLKQSCSTKYRTL 49
Dd	1 MILANAFCLPFLLDETIRSLASPSSLOGSELHGWRPVQDCVRANELCAEASNCSSRYTL 60
OY	50 RQCACGETNSLSLGLSEADCECSAMALKOKSLNCRCKRGKRGKCNLCRIYWSYQS 109
Dd	61 RQLAGDGDRNTML-----ANKECQALEVIOESPLYCRRCKRGKKELQCIQTYSIHLG 115
OY	110 L-QGNDDLEDSPEYPVNSRLSDIFRAVPFLSDVFQQVEHISKGNNCLDAKACNLDPDTC 168
Dd	116 LTBESEFPFVASPYEPVSRSLSDIFRLASIFSCTGTPDAVSTKSHGLCDAAKNLNDNCK 175
OY	169 KYRSAYITPCTTSS-N-EVCNRKRCKHALRPFKPAPAKSIYGLFSCGDIACERRQ 227
Dd	176 KLRSSYSISICREISPTERCRRKCHXALRQFFRPVSEYYTMLFCSCDDQCAERBRQ 235
OY	228 TIVVCGSEEBERENCCLSDOSCKTNVICSRDLDFPNOCOPBSRSVNCLEKENYAACL 287
Dd	236 TLPSCEYDEKEKNCCLDLRCLCTDYLCRSLADFLANCRASTRITTSCPADNYQCLG 295
OY	288 AYSGLIGVTMPNYVS--SSLVAWPWCDCSNSGNDLEDCLKPLNPKONTCLKNAIQAF 345
Dd	296 SYAAMIGFDMTPNVYDNSPTGITVSPMCNCRGSGMNEEECEKFLRDTENPCLNIAIQAF 355
OY	346 GNGSDVMQMGPAPRVQTTATTTAAPFYKXKPLGP--AGSENELPTHVLPPCANLQOXL 403
Dd	356 GNGTDVNMSPKGFPLPAIQAP----VKEKTPLLDPLSDSTSIGTSIVTTCTSIQOGL 410
OY	404 KSNTSGSTHLCLSDSDFGKDGLAGASHITTKMAAPSPCSLSLPVLMLT 454
Dd	411 KANNSKELSMCFTELTTNISPGSKVKIKLMSGSSRARLSAALTPLPLMLT 461
RESULT 12	
GFR2_MOUSE	
ID	GFR2_MOUSE STANDARD; PRT; 463 AA.
AC	008842;
DT	01-NOV-1997 (Ref. 35, Created)
DT	01-NOV-1997 (Ref. 35, Last sequence update)
DT	05-JUL-2004 (Ref. 44, Last annotation update)
Dd	GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin
Dd	receptor alpha) (NTRN-alpha) (NTRN-beta) (tGF-beta related
Dd	neurotrophic factor receptor 2) (GDNF receptor beta) (GDNFR-beta).
GN	Name=frf2; Synonym=Gdnfrb, Trn2;
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX	MEDLINE=g7325791; PubMed=9182803; DOI=10.1016/S0896-6273(00)80318-9;
RA	Balch R.H., Tansey M.G., Golden J.P., Creedon D.J., Heuckeroth R.O.,
RA	Keck C.L., Zimonjic D.B., Popescu N.C., Johnson E.M., Jr.,
RA	Malbrand J.,
RT	"Trn2, a novel receptor that mediates neurturin and GDNF signaling
RT	through Ret."
RL	Neuron 18:793-802(1997).
CC	-!- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced
CC	autophosphorylation and activation of the RET receptor. Also able
CC	to mediate GDNF signaling through the RET tyrosine kinase
CC	receptor.
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By

```
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=008842-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=008842-2; Sequence=VSP_001662;
CC -1- TISSUE SPECIFICITY: Neurons of the superior cervical and dorsal
CC root ganglia, and adult brain and testis. Low level in the spleen
CC and in the adrenal gland.
CC -1- SIMILARITY: Belongs to the GDNFR family.
CC -----
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CC -----
CC EMBL; AF002701; AAC53548.1; -.
CC MGD; MGI:1195462; Gfra2.
CC InterPro; IPR003438; GDNF_receptor.
CC Pfam; PF02351; GDNF; 1.
CC PRINTS; PR01316; GDNFRECEPTOR.
CC KX Alternative splicing; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
CC Receptor; Signal.
CC FT SIGNAL 1 21 Potential.
CC FT CHAIN 22 443 GDNF family receptor alpha 2.
CC FT PROPEP 444 463 Removed in mature form (Potential).
CC FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 357 357 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 413 413 N-linked (GlcNAc...) (Potential).
CC FT LIPID 443 443 GPI-anchor amidated serine (Potential).
CC FT VARSPDIC 14 146 Missing (in isoform 2).
CC FT FTId=VSP_001662.
CC SEQUENCE 463 AA; 51598 MW; 4FBA95F586C1F78 CRC64;
SO
Query Match 44.7%; Score 1112.5; DB 1; Length 463;
Best Local Similarity 47.6%; Pred. No. 1.4e-75;
Matches 224; Conservative 81; Mismatches 139; Indels 27; Gaps 9;
QY 1 MFAT---LYFAL--PLDLLMSAEVSGD-----RLDVKASDQCLKQSGSTYRTL 49
DB 1 MIANAFCLEFFLDETLRLASPSPOGSEIHGMRPQVDCVRANHELCAAESNCSRYRTL 60
QY 50 ROCVAGKETPFLSTGLEAKDECRSMEALKOKSLVNCRCRGMKKKCNCLRIYWSYOS 109
DB 61 RQCLAGRDNTML-----ANKECQALAEVLQESPLDCKCRGMKKELQCLQIYWSIHG 115
QY 110 L-QGNDLLEDSPEYPVNSRLSDIFRAVPFISDFQOVEHISKNNCLDAKACNLDCTCK 168
DB 116 LTGEFEFYSAPYEPYTSRLSDIFRLASIFSGTADPVVASAKNHCLDAKACNLDNCK 175
QY 169 KYRSAYITTCSTMS-NEVCNRRKCHKALROFPDKVPAAKSYGLMFCSCDIACTERRQ 227
DB 176 KRRSSYISICNREISPTERCNRKCHKALROFPDRVSEYTYRMLFSCCODQCAERRQ 235
QY 228 TIIVPVSSEBERPNCISLQDSCKTYICRSRLADFTTNCOPRSVSNCLKENYADCLL 287
DB 236 TIIPSCSYEDKEKPNCLDLRLCRTHLGRSLADFHANCRASRYRTITSCPDANYQAICG 295
QY 288 AVSGLIGTWTPNYVDS--SSLVAWPWCDCNSGNDLECLKFLNFKONTCLKNAIOAF 345
DB 296 SYAGMIGFMTPTVYVDSNPTGIIVSPWCNCRSGNNEECEKFLKDPFTPCRNIAIOAF 355
QY 346 GNSDVTVMOPAPVQTTATTTTAFVKNKPLGP--ASEBNEIPHYVLPCCANLQAOXL 403
DB 356 GNGTDVNMSPKGP-----TFSATQAPRVEKTPSLPDLSDSTLIGTSVITTCSTIOEGL 410
QY 404 KSNVSGSTHCLTSDSPFGKDLGASGSHITTKSMAAPSPCSLSLPVLMLT 454
DB 411 KANNSKEISLSCFTBLTNTISPSGSKYIKLYSSGCRALSTALTALPLAMWT 461
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RESULT 13
ID Q920Y3 PRELIMINARY; PRT; 463 AA.
AC Q920Y3;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Glial cell line derived neurotrophic factor family receptor alpha
DE 2.
OS Name=Gfra2;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RX MEDLINE=22712886; PubMed=12829325; DOI=10.1016/S0169-328X(03)00169-4;
RA Too H.P.;
RT "Real time PCR quantification of GFRalpha-2 alternatively spliced
RT isoforms in murine brain and peripheral tissues."
RL Brain Res. Mol. Brain Res. 114:146-153(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Wong Y.W.; Too H.P.;
RL EMBL; AF398416; AAK97483.1; to the EMBL/GenBank/DBJ databases.
DR EMBL; AF398411; AAK97483.1; JOINED.
DR EMBL; AF398412; AAK97483.1; JOINED.
DR EMBL; AF398414; AAK97483.1; JOINED.
DR EMBL; AF398415; AAK97483.1; JOINED.
DR EMBL; AF398413; AAK97483.1; JOINED.
DR GO; GO:0004872; F:receptor activity; IEA.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01316; GDNFRECEPTOR.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SO SEQUENCE 463 AA; 51582 MW; 42FAA1EF59975E2C CRC64;
QY 1 MFAT---LYFAL--PLDLLMSAEVSGD-----RLDVKASDQCLKQSGSTYRTL 49
DB 1 MIANAFCLEFFLDETLRLASPSPOGSEIHGMRPQVDCVRANHELCAAESNCSRYRTL 60
QY 50 ROCVAGKETPFLSTGLEAKDECRSMEALKOKSLVNCRCRGMKKKCNCLRIYWSYOS 109
DB 61 RQCLAGRDNTML-----ANKECQALAEVLQESPLDCKCRGMKKELQCLQIYWSIHG 115
QY 110 L-QGNDLLEDSPEYPVNSRLSDIFRAVPFISDFQOVEHISKNNCLDAKACNLDCTCK 168
DB 116 LTGEFEFYSAPYEPYTSRLSDIFRLASIFSGTADPVVASAKNHCLDAKACNLDNCK 175
QY 169 KYRSAYITTCSTMS-NEVCNRRKCHKALROFPDKVPAAKSYGLMFCSCDIACTERRQ 227
DB 176 KRRSSYISICNREISPTERCNRKCHKALROFPDRVSEYTYRMLFSCCODQCAERRQ 235
QY 228 TIIVPVSSEBERPNCISLQDSCKTYICRSRLADFTTNCOPRSVSNCLKENYADCLL 287
DB 236 TIIPSCSYEDKEKPNCLDLRLCRTHLGRSLADFHANCRASRYRTITSCPDANYQAICG 295
QY 288 AVSGLIGTWTPNYVDS--SSLVAWPWCDCNSGNDLECLKFLNFKONTCLKNAIOAF 345
DB 296 SYAGMIGFMTPTVYVDSNPTGIIVSPWCNCRSGNNEECEKFLKDPFTPCRNIAIOAF 355
QY 346 GNSDVTVMOPAPVQTTATTTTAFVKNKPLGP--ASEBNEIPHYVLPCCANLQAOXL 403
DB 356 GNGTDVNMSPKGP-----TFSATQAPRVEKTPSLPDLSDSTLIGTSVITTCSTIOEGL 410
```

QY 404 KSNVSGSTHLCISDSDFGKDLGASGSHITTKSMAPSCSISLPLVMT 454
 DB 411 KANNKSKELSMCFTELTTNISPSGSKVITLXSGSCARLSTALTALPLVMT 461

RESULT 14

GFR2_HUMAN STANDARD: PRT; 464 AA.
 ID GFR2_HUMAN
 AC 000451; O15316; O15328;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin receptor alpha) (NTR-alpha) (NRTN-alpha) (TGF-beta related neurotrophic factor receptor 2) (GDNF receptor beta) (GDNFR-beta) (RET ligand 2).
 DE Name=GFR2; Synonyms=GDNFR, RETL2, TRNR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=97325791; PubMed=9182803; DOI=10.1016/S0896-6273(00)80318-9; RA Balch R.H., Tansey M.G., Golden J.P., Crendon D.J., Heuckeroth R.O., Reck C.L., Zimonjic D.B., Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
 RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling through Ret.";
 RL Neuron 18:793-802(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=97402208; PubMed=9259272; DOI=10.1093/mmg/6.8.1267; RA Svantco P., Martiovaara K., Lindahl M., Artuue U., Moshayakov M., Horelli-Kuitanen M., Aitakainen M.S., Palotie A., Saxiöla H., Saarna M.;
 RT "Cloning, mRNA distribution and chromosomal localisation of the gene for glial cell line-derived neurotrophic factor receptor beta, a homologue to GDNFR-alpha.";
 RL Hum. Mol. Genet. 6:1267-1273(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RX MEDLINE=97322356; PubMed=9177201; DOI=10.1073/pnas.94.12.6238; RA Sanicola M., Hession C.A., Worley D.S., Camillo P., Ehrenfeld C., Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitty A., Pepinsky R.B., Cate R.B.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 CC -1- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced autophosphorylation and activation of the RET receptor. Also able to mediate GDNF signaling through the RET tyrosine kinase receptor.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=000451.1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=000451.2; Sequence=VSP_001661;
 CC -1- SIMILARITY: Belongs to the GDNFR family.
 CC -1- TISSUE SPECIFICITY: Isoform 1 is found in both brain and placenta.
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 CC -----
 CC EMBL: AF002700; AAC52036.1; -
 CC DR EMBL: U93703; AAB61922.1; -
 CC DR EMBL: U97145; AAC51647.1; -
 CC DR Genew; HGNC:4244; GFR2.
 CC MIM; 601956; -
 CC DR GO; GO:0019898; C:extrinsic to membrane; TAS.
 CC DR GO; GO:0016167; P:glial cell line-derived neurotrophic factor . . ; TAS.
 CC DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; TAS.
 CC DR InterPro; IPR003438; GDNF_Receptor.
 CC DR Pfam; PF02351; GDNF; 1.
 CC DR PRINTS; PR01316; GDNFRRECEPTOR.
 CC KW Alternative splicing; Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
 CC FT SIGNAL 1 21 Potential.
 CC FT CHAIN 22 44 GDNF family receptor alpha 2.
 CC FT PROPE 445 464 Removed in mature form (Potential).
 CC FT CARBOHYD 52 52 N-linked (GlcNAc . . .) (Potential).
 CC FT CARBOHYD 357 357 N-linked (GlcNAc . . .) (Potential).
 CC FT CARBOHYD 413 413 N-linked (GlcNAc . . .) (Potential).
 CC FT LIPID 444 444 GPI-anchor amidated serine (Potential).
 CC FT VARSPLIC 14 146 Missing (in isoform 2).
 CC FT CONFLICT 6 6 /Ftd=VSP_001661.
 CC FT CONFLICT 462 462 V -> A (in Ref. 2).
 CC FT SEQUENCE 464 AA; 51558 MM; 88C604D9530FF21F CRC64;
 CC SQ

Query Match 44.6%; Score 1109.5; DB 1; Length 464;
 Best Local Similarity 47.9%; Pred. No. 2,46-75;
 Matches 226; Conservative 76; Mismatches 139; Indels 31; Gaps 10;

QY 1 MFLATYFALPLD-----LMSAEVSG-GDRLDCKVAKSDOCLKESQSTKXRTL 49
 DB 1 MILANVFLFFFLBETTLASLPSSLGQPELHGRRPPVDCVRAELCAASNCSSKRTIL 60
 QY 50 RQCVAGKETNFSLTSGLEAKDECRSAMBALKOKSLYNCRCRCKGKKEKNCRLRTYSWYQS 109
 DB 61 RQCLAGRRNMTL-----ANKEQALLEVLDQESPLVYCRCKRGKKEKLCGLQITWSTHLG 115
 QY 110 L-QGNDLLEDSPPYEPVNSRLSDITFRANVFTSDVQVQVEHLSKGNCLDAKACMLDPTCK 168
 DB 116 LTBGEFEFEASPPYVPVSRSLSDIFRLASIFSGTGADPVVSAKSHCLDAKACMLDNCK 175
 QY 169 KYRSAYITPCTTSS-NEVCNRKCHALRQFPDVKAKSHYGLFQSCDICTERRRQ 227
 DB 176 KLRSSYISICREISPTERCNRKCHALRQFPDVKSEYTRMLFSCDQQAERRRQ 235
 QY 228 TIVPVCSYEEREPNCLSLDSCRTNYICRSRLADFTNCQPSRSVSNCLKENYADCLL 287
 DB 236 TILPSCSYEDKEXNCLDLRGVCRTHDLCSRLADFPANCRASQYVITSCPADNYQACLG 295
 QY 288 AYSGLIGTVMTPNYVDS--SLSYAPWCDCSNGNDLEDCLKFLNFKDNTCLKNAIQAF 345
 DB 296 SYAGMIGPDMTPNYVDSPTGIIVSPWCSCGSGNMEEECEKFLRDPENPCRLNAIQAF 355
 QY 346 GNGSGVYVMQAPVQVTTATTTAFVYKPKLGP--AGSENEPHTVLPFCANLQAK 403
 DB 356 GNGTDVNVSPKGFQAOAP-----VREKTPSLPDDLSDTSGTSTGTSVITTCVSQOGL 410
 QY 404 KSNVSGSTHLCISDSDFGKDLGASGSHITTKS--MAAPSCSISLPLVMT 453
 DB 411 KANNKSKELSMCF--TELTTNIPSNSKVITKENSQPSARRSALTIVSLVMT 460

RESULT 15
 QY 0792X9 PRELIMINARY: PRT; 444 AA.
 AC 0792X9;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE GDNF receptor-beta (Fragment).

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=97402208; PubMed=9259272; DOI=10.1093/hmg/6.8.1267;
RA Suvanto P., Wartiovaara K., Lindahl M., Arumae U., Moshnyakov M.,
RA Horelli-Kuitunen N., Aliraksinen M.S., Palotie A., Sariola H.,
RA Saarna M.;
RT "Cloning, mRNA distribution and chromosomal localisation of the gene
RT for glial cell line-derived neurotrophic factor receptor beta, a
RT homologue to GDNFR-alpha.";
RL Hum. Mol. Genet. 6:1267-1273(1997).
DR EMBL; AF003825; AAD09310.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptor2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PRO1318; GDNFRALPHA2.
DR PRINTS; PRO1316; GDNFRECEPTOR.
DR Receptor.
KM Receptor.
SQ SEQUENCE 444 AA; 49578 MW; A548644EDB36D5F3 CRC64;
FT NON TER 444
SQ
Query Match 44.2%; Score 1098.5; DB 2; Length 444;
Best Local Similarity 49.3%; Pred. No. 1.5e-74;
Matches 214; Conservative 74; Mismatches 119; Indels 27; Gaps 9;
QY 1 MFLAT---LYFAL-PLDLMSAFVSGD-----RLDVKASDQCKEQSCTKYRTL 49
DB 1 MILANAFCLFFLDERTSLASPSLQSGSLHGMRPQVDCVRANELCAEBSNCSRYRTL 60
QY 50 ROCVAKETFTSLTSGLEAKDECRSAMEALQKSLVNCRCRGKKEKNCRLTYMSWYQS 109
DB 61 RQCLAGRDNRMTL-----ANKECALAEVYQESPLDRCRKMKELQCLQIYMSIHG 115
QY 110 L-QGNDLLEDSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNNCIDAAKACNLDTCK 168
DB 116 LTEGEEFYEASPYEPTYSRLSDIFRLASIFSGTDPAVSTKSNHCLDAKACNLNDCK 175
QY 169 KYRSATITPCTTMS-NEVGNRRKCHKALQFPDKVPAKHSYGMFLFCSCRDIACTERRQ 227
DB 176 KLRSSYISICNREISPTERCNRKCHKALQFPDRVSEYTYMLFSCCODAACARRRQ 235
QY 228 TIYPVCSYEERBRPNCLSDOSCKTNYICRSRLADFFTNCOEPSRSVSNCKENYVADCLL 287
DB 236 TILPSCSYEDKEKNCILDRLSLCRTDHLCSRLADFHANCRASYRTITSCPADNYQACLG 295
QY 288 AVSGLIGTWTPTNYVDS--SSLVAPWCDCSNSGNDLEDCLKPLNFKDNTCLKNAIQAF 345
DB 296 SYAGMIGFDMTPNYVDSNPTGIIVSPWCMCRSGNMEBECEKFLRDPTENPCLRNAIQAF 355
QY 346 GNGSDVTMMQAPAPVQTTATTTTARVKKPLGP--AGSENEIPTHVLPCCANLQAKL 403
DB 356 GNGTDVNMSPKGSPLATQAP-----RVKETSPLPDDLSDSTSLGTSVITTTCTSIQOGL 410
QY 404 KSNVSGSTHCLSD 417
DB 411 KANNSEKELSMCTFE 424

Search completed: February 17, 2005, 09:43:55
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:14 ; Search time 80 Seconds
(without alignments)
2262.548 Million cell updates/sec

Title: US-10-033-350-2

Sequence: 1 MFLLATLTPALPILDLMSAE.....PYLMTALALISVSLAETS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_16Dec04:.*
2: geneseqp1908:.*
3: geneseqp1908:.*
4: geneseqp2000s:.*
5: geneseqp2001s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468	100.0	468	2	AAW35334 Rat glial
2	2468	100.0	468	2	AAW27327 Rat glial
3	2468	100.0	468	2	AAW37457 Rat Ret 1
4	2468	100.0	468	2	AAW84164 Glial cel
5	2468	100.0	468	7	ADDI1672 Rat glial
6	2468	100.0	468	7	ADDE60800 Rat Prote
7	2468	100.0	468	7	ADDA6323 Rat Prote
8	2468	100.0	468	8	ADJ58694 Rat RetL1
9	2472	99.4	468	2	AAW92298 Rat GDNFR
10	2316.5	93.1	465	2	AAW35333 Human gl1
11	2316.5	93.1	465	2	AAW84163 Glial cel
12	2316.5	93.1	465	5	ABJ05547 Breast ca
13	2316.5	93.1	465	7	ADDI1673 Human gl1
14	2316.5	93.1	465	7	ADDA6325 Human Pro
15	2316.5	93.1	465	7	ADDE60802 Human Pro
16	2316.5	93.1	465	7	ADN38766 Cancer/an
17	2311.5	92.9	463	2	AAW84167 GDNFR-ald
18	2309.5	92.8	465	2	AAW84165 GDNFR-ald
19	2306.5	92.7	463	2	AAW84166 GDNFR-ald
20	2306.5	92.7	465	2	AAW92300 Human GDN
21	2278	91.6	460	2	AAW37459 Human Ret
22	2278	91.6	460	3	AAW15175 Human GFR
23	2278	91.6	460	6	ABP97180 Tumour-as
24	2278	91.6	460	8	ADJ58703 Human ret
25	1686	67.8	346	2	AAW37458 Human Ret

26	1686	67.8	346	8	ADJ58701 Human ret
27	1431.5	57.5	294	2	AAW84169 GDNFR-ald
28	1220	49.0	232	2	AAW84168 GDNFR-ald
29	1176.5	47.3	498	2	AAW84183 Consensus
30	1120.5	45.0	464	2	AAW71602 Rat neut
31	1120.5	45.0	464	2	AAW92299 Rat GDNFR
32	1120.5	45.0	464	3	AAW80122 Rat neut
33	1120.5	45.0	464	5	ABW79036 Rat neut
34	1120.5	45.0	464	5	ABW09630 Amino aci
35	1120.5	45.0	464	5	AAU79266 Rat neut
36	1120.5	45.0	464	7	ADDI1657 Rat neut
37	1120.5	45.0	464	7	ADDE54591 Rat Prote
38	1120.5	45.0	464	7	ADDE63251 Rat Prote
39	1118.5	45.0	460	2	AAW84181 A GDNFR-a
40	1117.5	44.9	464	2	AAW71601 Human neu
41	1117.5	44.9	464	3	AAW15176 Human GFR
42	1117.5	44.9	464	3	AAW80121 Human neu
43	1117.5	44.9	464	5	ABW79035 Human neu
44	1117.5	44.9	464	5	ABW09629 Amino aci
45	1117.5	44.9	464	5	AAU79265 Human neu

ALIGNMENTS

RESULT 1	
AAW35334	AAW35334 standard; protein; 468 AA.
XX	
AC	AAW35334;
XX	
DT	01-MAY-1998 (first entry)
XX	
DE	Rat glial cell line-derived neurotrophic factor receptor.
XX	
KW	Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
KW	treatment; dopaminergic nerve cell disorder; Parkinson's disease;
KW	Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
KW	Huntington's disease; glaucoma; retinal degeneration; hearing loss;
KW	gene therapy.
XX	
OS	Rattus sp.
XX	
PN	MO9740152-A1.
XX	
PD	30-OCT-1997.
XX	
PF	15-APR-1997; 97WC-US006281.
XX	
PR	22-APR-1996; 96US-0015907P.
PR	09-MAY-1996; 96US-0017221P.
PR	14-APR-1997; 97US-00837199.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Fox GW, Wen D, Jing S;
XX	
DR	WPI; 1997-535836/49.
XX	
DR	N-PSDB; AAT95297.
PT	Glial cell line derived neurotrophic factor receptor - useful to treat
PT	dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
XX	disease.
PS	Claim 1; Page 96-98; 196pp; English.
XX	
CC	The present sequence is the rat glial cell line-derived neurotrophic
CC	factor (GDNF) receptor, which can be used to treat dopaminergic nerve
CC	cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic
CC	lateral sclerosis, complications of diabetes and Huntington's disease and
CC	(optionally in combination with GDNF) glaucoma, retinal degeneration and
CC	hearing loss caused by injury to inner ear sensory neurons. The receptor
CC	can also be used to block unwanted GDNF activity; analyse GDNF related

CC molecules and stabilise GDNF in pharmaceutical formulations. Receptor
 CC expressing cells, preferably transfected ex vivo, can be used similarly
 CC by implantation, and the use of the receptor cDNA in gene therapy is also
 CC contemplated. Probes based on the cDNA can be used to identify GDNF
 CC responsive cells and tissues, e.g. to identify patients who would benefit
 CC from GDNF therapy, and abnormalities in receptor expression, and to
 CC isolate molecules that form a complex with the cDNA or are
 CC homologous/cross-reactive with the cDNA. Anti-receptor antibodies,
 CC oligonucleotides derived from the cDNA and animal models that overexpress
 CC the receptor can be used to study the biological function of GDNF,
 CC knockout transgenic animals can be used to detect GDNF dependent neurons
 CC or processes and the antibody can be used in immunoassays for the
 CC receptor. The receptor binds GDNF specifically and with high affinity,
 CC acting as part of a complex that mediates/enhances signal transduction by
 CC GDNF, i.e. increasing dopamine uptake in dopaminergic cells

XX Sequence 468 AA;

Query Match 100.0%; Score 2488; DB 2; Length 468;

Best Local Similarity 100.0%; Pred. No. 4.4e-199; Mismatches 0; Indels 0; Gaps 0;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLATLYPALDLILMSAEVSGGDRLDVAVASDQCKEKGSCSTYRTLRQCVAKETNF 60
 DB 1 MFLATLYPALDLILMSAEVSGGDRLDVAVASDQCKEKGSCSTYRTLRQCVAKETNF 60
 QY 61 SLTSGLEAKDECRAMEALKOKSLYNCRCKGKMKERKCLRTYMSYQSLQNDLLEDSF 120
 DB 61 SLTSGLEAKDECRAMEALKOKSLYNCRCKGKMKERKCLRTYMSYQSLQNDLLEDSF 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDTCCKYRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDTCCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHAKALRQFPDKVPKASGYGMFSCCRDIACERRRQITVPCSYEBER 240
 DB 181 SMSNEVCNRRCKHAKALRQFPDKVPKASGYGMFSCCRDIACERRRQITVPCSYEBER 240
 QY 241 PNCISLQDSCKTNYICRSLADFPNQCPESSVSNCLKENYADCLLAVSGLIGVTMPN 300
 DB 241 PNCISLQDSCKTNYICRSLADFPNQCPESSVSNCLKENYADCLLAVSGLIGVTMPN 300
 QY 301 YVSSSSLSVAPWCDCNSGNDLEDCIKFLNFKDNTCKNAIQAFGNGSDVTMPAPPV 360
 DB 301 YVSSSSLSVAPWCDCNSGNDLEDCIKFLNFKDNTCKNAIQAFGNGSDVTMPAPPV 360
 QY 361 QTTTATTTTARVRVKKPLGPAGSENEIPTHVLPICANLQAOKLKSNVSGSTHLCSDSD 420
 DB 361 QTTTATTTTARVRVKKPLGPAGSENEIPTHVLPICANLQAOKLKSNVSGSTHLCSDSD 420
 QY 421 GKDGLAGASHITTKSMAPPSCSLSLPIVMTLTAALLSYLAETS 468
 DB 421 GKDGLAGASHITTKSMAPPSCSLSLPIVMTLTAALLSYLAETS 468

RESULT 2

AAW27327 standard; protein; 468 AA.

AAW27327;

27-APR-1998 (first entry)

Rat glial cell derived neurotrophic factor receptor alpha.

Glia1 cell derived neurotrophic factor receptor alpha; GDNFR alpha; GDNF;
 rat; kidney disease; glomerulonephritis; therapy.

Rattus sp.

Key Location/Qualifiers
 1..24
 Peptide /label= sig_peptide

FT

FT Domain 25..445
 FT /note= "extracellular domain"
 FT Modified-site 61
 FT /note= "O-glycosylated"
 FT Modified-site 349
 FT /note= "O-glycosylated"
 FT Modified-site 408
 FT /note= "O-glycosylated"
 FT Cleavage-site 428..430
 FT /note= "GPI-anchor cleavage/attachment site"
 FT Domain 446..468
 FT /note= "GPI-attachment site"
 PD MO9733912-A2.
 PD 18-SEP-1997.
 PF 13-MAR-1997; 97WO-US004363.
 PF 14-MAR-1996; 96US-00615902.
 PR 14-MAR-1996; 96US-00618236.
 XX (GETH) GENENTECH INC.
 PA Klein RD, Moore MW, Rosenthal A, Ryan AM,
 PI MPI. 1997-470819/43.
 DR N-PSDB; AAT84975.
 DR Isolated glial cell derived neurotrophic factor receptor alpha - useful
 PT to develop products to diagnose and treat associated disorders,
 PT particularly enteric nervous system or kidney disorders.
 PS Claim 1; Page 78-79; 100pp; English.

This protein comprises full-length rat glial cell derived neurotrophic factor receptor alpha (GDNFR alpha), a novel GPI-linked protein that is a ligand-binding component of the receptor system for GDNF. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT84975). The invention relates to novel uses of GDNF and its receptor. In particular, it relates to native rat GDNFR alpha (see AAW27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antibodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, CC systems for studying the physiological role of GDNF, diagnostic CC techniques for identifying GDNF-related conditions, methods for CC identifying molecules homologous to GDNFR alpha, and therapeutic CC techniques (claimed) for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with CC glomerulonephritis and enteric nervous system related disorders. CC Transgenic and knockout animals are also claimed

Sequence 468 AA;

Query Match 100.0%; Score 2488; DB 2; Length 468;

Best Local Similarity 100.0%; Pred. No. 4.4e-199; Mismatches 0; Indels 0; Gaps 0;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLATLYPALDLILMSAEVSGGDRLDVAVASDQCKEKGSCSTYRTLRQCVAKETNF 60
 DB 1 MFLATLYPALDLILMSAEVSGGDRLDVAVASDQCKEKGSCSTYRTLRQCVAKETNF 60
 QY 61 SLTSGLEAKDECRAMEALKOKSLYNCRCKGKMKERKCLRTYMSYQSLQNDLLEDSF 120
 DB 61 SLTSGLEAKDECRAMEALKOKSLYNCRCKGKMKERKCLRTYMSYQSLQNDLLEDSF 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDTCCKYRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDTCCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHAKALRQFPDKVPKASGYGMFSCCRDIACERRRQITVPCSYEBER 240
 DB 181 SMSNEVCNRRCKHAKALRQFPDKVPKASGYGMFSCCRDIACERRRQITVPCSYEBER 240

DB 181 SMSNEVCNRKCKHAKLROFFDKVPAGHSYGMFLFCSGRDIACRERRRQTIIVPVCSEERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAAYSGLLGTWTPN 300
 DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAAYSGLLGTWTPN 300
 QY 301 YDSSSLSYAPWPCDCNSGNDLEDCLKFPLNFKDNTCLKNAIOAFNGSGSVTMQAPAPV 360
 DB 301 YDSSSLSYAPWPCDCNSGNDLEDCLKFPLNFKDNTCLKNAIOAFNGSGSVTMQAPAPV 360
 QY 361 QTTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHCLSDSD 420
 DB 361 QTTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHCLSDSD 420
 QY 421 GKDGLAGASSHITTKSMAAPPSCSLSLPVLMTLAALLSVLAETS 468
 DB 421 GKDGLAGASSHITTKSMAAPPSCSLSLPVLMTLAALLSVLAETS 468

RESULT 3
 AAW37457
 ID AAW37457 standard; protein; 468 AA.
 XX
 AC AAW37457;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Rat Ret ligand RetL1.
 XX
 KM Ret ligand; RetL1; receptor; signal transduction; rat; cell growth;
 KM renal cell; hypoxic injury; neurodegeneration; motor neurone disease;
 KM toxic injury; hypoxic injury; nephritis; kidney transplant;
 KM multiple sclerosis; infection; meningitis; myelopathy;
 KM Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury;
 KM Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
 KM myasthenia gravis; tumour; therapy.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= Sig_peptide
 XX
 PN MO9744356-A2.
 XX
 PD 27-NOV-1997.
 XX
 PF 07-MAY-1997; 97MO-US007726.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 11-APR-1997; 97US-0043533P.
 XX
 PA (Bio) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL;
 XX
 DR WPI; 1998-018431/02.
 DR N-PSDB; AAV00245.
 XX
 PT New nucleic acid encoding ret receptor ligands and related proteins -
 PT vectors, transformed cells and antibodies, used for promoting cell growth
 PT and improving survival of injured cells, especially renal or nerve cells.
 XX
 PS Claim 2; Page 49-51; 113pp; English.
 XX
 CC This protein comprises rat Ret ligand (RetL1) RetL1, a key component of
 CC the Ret signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of the
 CC Ret tyrosine kinase domain. The amino acid sequence was deduced from a
 CC cDNA clone (see AAV00245) obtained from a rat embryonic kidney cDNA
 CC expression library. Human RetL1 as well as mouse and human RetL2 and

CC RetL2 sequences have also been identified (see AAW37458-63). Vectors
 CC containing retL1 DNA and prokaryotic or eukaryotic host cells transformed
 CC or transfected with these vectors are claimed, as well as a method for
 CC production of RetL1, its soluble variants (e.g. amino acids 1-434) and
 CC fusion proteins with a toxin, imageable compound or radionuclide. RetL1,
 CC optionally when expressed from vectors in vivo, is used to promote growth
 CC of new tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure, nephritis,
 CC kidney transplants, toxic or hypoxic injury, neurodegeneration, motor
 CC neurone disease, multiple sclerosis, bacterial, viral or prion infections
 CC (e.g. meningitis, myelopathy associated with HIV or Creutzfeldt-Jakob
 CC disease), cranial nerve or spinal cord injury, developmental disorders
 CC such as Down's syndrome and cerebral palsy, or conditions involving the
 CC peripheral nervous system (Lyme disease, muscular dystrophy and
 CC myasthenia gravis). Fusion proteins are used to deliver toxins etc. to
 CC Ret-expressing cells, especially tumours
 CC
 SQ Sequence 468 AA;
 Query Match 100.0%; Score 248; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFPLATYFALPLDLMSAEVSGDRIDCYKASDOCLKEQSCSTKYRTLRQYAGKETNF 60
 DB 1 MFPLATYFALPLDLMSAEVSGDRIDCYKASDOCLKEQSCSTKYRTLRQYAGKETNF 60
 QY 61 SLTSGLEADECRSAMEALKQKSLVNCRCRGMKKEKNCRIYMSYQSLQGNDLLEDS 120
 DB 61 SLTSGLEADECRSAMEALKQKSLVNCRCRGMKKEKNCRIYMSYQSLQGNDLLEDS 120
 QY 121 YEVNRLSDIPRAVPFIDVFOQVHISKNNCLDAACNLDPTCKKRSAYITPCTT 180
 DB 121 YEVNRLSDIPRAVPFIDVFOQVHISKNNCLDAACNLDPTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRKCKHAKLROFFDKVPAGHSYGMFLFCSGRDIACRERRRQTIIVPVCSEERER 240
 DB 181 SMSNEVCNRKCKHAKLROFFDKVPAGHSYGMFLFCSGRDIACRERRRQTIIVPVCSEERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAAYSGLLGTWTPN 300
 DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAAYSGLLGTWTPN 300
 QY 301 YDSSSLSYAPWPCDCNSGNDLEDCLKFPLNFKDNTCLKNAIOAFNGSGSVTMQAPAPV 360
 DB 301 YDSSSLSYAPWPCDCNSGNDLEDCLKFPLNFKDNTCLKNAIOAFNGSGSVTMQAPAPV 360
 QY 361 QTTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHCLSDSD 420
 DB 361 QTTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHCLSDSD 420
 QY 421 GKDGLAGASSHITTKSMAAPPSCSLSLPVLMTLAALLSVLAETS 468
 DB 421 GKDGLAGASSHITTKSMAAPPSCSLSLPVLMTLAALLSVLAETS 468

RESULT 4
 AAW84164
 ID AAW84164 standard; protein; 468 AA.
 XX
 AC AAW84164;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Glial cell-line derived neurotrophic factor receptor-alpha protein.
 XX
 KM Rat; glial cell-line derived neurotrophic factor receptor-alpha;
 KM GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KM neurotrophin; signal transduction; dopaminergic nerve cell;
 KM Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KM neurological disorder; diabetes; glaucoma; sensory neuron;
 KM retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
 KM gene therapy.

Query Match	100.0%;	Score 2488;	DB 2;	Length 468;
Best Local Similarity	100.0%;	Pred. No. 4,4e-199;		
Matches 468;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
1	MLATLTYPALPLTDLILMSAEVSGGDRLLDCVKASDQCLTKKOSOSTKYRTLROCVAGKEITNF	60		
1	MLATLTYPALPLTDLILMSAEVSGGDRLLDCVKASDQCLTKKOSOSTKYRTLROCVAGKEITNF	60		
61	SLTSGLEAEDERSAMEALKOKSLVNCRCRKGMKEKCNCLRIYWSMYOSLGNDLLEDSF	120		
61	SLTSGLEAEDERSAMEALKOKSLVNCRCRKGMKEKCNCLRIYWSMYOSLGNDLLEDSF	120		
121	YEPVNSRLSDIFRAVPFISDVFOVEHISKANNCLDAAYACMLDTCCKYRSAYITPCTT	180		
121	YEPVNSRLSDIFRAVPFISDVFOVEHISKANNCLDAAYACMLDTCCKYRSAYITPCTT	180		
161	SMSNVECNRRKCHKALROFEPDVPAGHSGMLFCGSRDILACTERRRQOTIVPVCSEERR	240		
161	SMSNVECNRRKCHKALROFEPDVPAGHSGMLFCGSRDILACTERRRQOTIVPVCSEERR	240		

Oy		241	PNCISLSDSCKTNVIGRSLADPFNNCOPESSVSANCLKENYADCCLLAYSGLIGTWTPN	300
Oy		241		
Dd		241	PNCISLSDSCKTNVIGRSLADPFNNCOPESSVSANCLKENYADCCLLAYSGLIGTWTPN	3000
Oy		301	YVDSSLSVAWPCDCSNGNDLEDCLKFLNFPKDNTCLKNAIQAFGNGSDVTMMQPAAPV	366
Dd		301	YVDSSLSVAWPCDCSNGNDLEDCLKFLNFPKDNTCLKNAIQAFGNGSDVTMMQPAAPV	366
Oy		361	QTATTATTTTFRVKANKPLGPAGSENEIPRHVLPPCANIQAKLSNVSGSTHLLCSDSDF	420
Dd		361	QTATTATTTTFRVKANKPLGPAGSENEIPRHVLPPCANIQAKLSNVSGSTHLLCSDSDF	420
Oy		421	GKDGLAGASHITTKSMAAPSPCSSLSPVLMLTLTAALLSVSLAETS 468	
Dd		421	GKDGLAGASHITTKSMAAPSPCSSLSPVLMLTLTAALLSVSLAETS 468	
RESULT 5				
ID	ADD11672			
XX	ADD11672	standard; protein; 468 AA.		
AC	ADD11672;			
XX				
DT	01-JAN-2004	(first entry)		
XX				
DE	Rat glial cell line derived factor receptor alpha.			
XX				
KW	Rat; Neurturin receptor alpha; NTNRA1pha; receptor; antiparkinsonian;			
KW	nocitropic; neuroprotective; antididiabetic; cytokine; neurotrophic factor;			
KW	gene therapy; amyotrophic lateral sclerosis; diabetes;			
KX	Parkinson's disease; Alzheimer's disease;			
KW	glial cell line derived factor receptor alpha; GDNFRA1pha.			
OS	Rattus norvegicus.			
XX				
FH	Key	Location/Qualifiers		
FT	Peptide	1..24		
FT		/note="Signal peptide"		
FT	Protein	25..468		
FT		/note="Mature GDNFRA1pha"		
XX				
PN	US2003110525-A1.			
PD	12-JUN-2003.			
XX				
PF	03-FEB-2003; 2003US-00357822.			
XX				
PR	18-FEB-1997; 97US-0038839P.			
PR	09-JUN-1997; 97US-0049818P.			
PR	24-OCT-1997; 97US-0063258P.			
PR	17-FEB-1998; 98US-00024655.			
PR	01-SEP-1999; 99US-00388316.			
XX				
PA	(KLEI/) KLEIN R D.			
PA	(ROSE/) ROSENTHAL A.			
PA	(HYNE/) HYNES M A.			
PI	Klein RD, Rosenthal A, Hynes MA;			
XX				
DR	WPI; 2003-810859/76.			
DR	N-PSDB; ADD11671.			
PT	New human neurturin receptor-alpha polypeptide useful for identifying a			
PT	compound that binds to or activates it, potentially useful as a			
PT	therapeutic.			
XX				
PS	Example 1; SEQ ID NO 21; 83bp; English.			
CC	The invention relates to a polypeptide comprising a sequence that is a			
CC	human neurturin receptor (NTNR)alpha extracellular domain or an allelic			
CC	variant of mammalian homologue of NTNRA1pha. Also include are an antibody			
CC	that specifically binds to NTNRA1pha, an isolated nucleic acid encoding			

CC NTNralpha, an expression vector comprising the nucleic acid, a host cell
 CC comprising the vector and a non-human transgenic animal which contains
 CC cells that express the nucleic acid to produce NTNralpha, (or which
 CC contains cells having an altered NTNralpha gene). The NTNralpha protein
 CC may comprise mature NTNralpha conjugated with, or fused to, a molecule
 CC which increases its serum half-life (e.g. IgG Fc or an IgG salvage
 CC receptor binding epitope). NTNralpha is used to identify a molecule which
 CC binds to or activates it, to purify a molecule which binds to it and to
 CC modulate a physiological response of a cell to neurotrophin. Soluble
 CC NTNralpha or soluble glial cell line derived factor alpha (GDNFRalpha) is
 CC used for activating Ret on the surface of a cell. An antibody that binds
 CC to NTNralpha is used in a composition that further comprises a cytokine
 CC or a neurotrophic factor. The antibody is also used to determine the
 CC presence of NTNralpha in a test sample. An agonist antibody to NTNralpha
 CC is used for activating NTNralpha in a cell. A nucleic acid encoding
 CC NTNralpha is used to produce NTNralpha by culturing a host cell and
 CC recovering NTNralpha. A nucleic acid that encodes NTNralpha or antisense
 CC nucleic acid that inhibits expression of NTNralpha can be used in gene
 CC therapy. Examples of diseases that can be treated are amyotrophic lateral
 CC sclerosis, diabetes, Parkinson's disease, and Alzheimer's disease. The
 CC present sequence represents rat glial cell line derived factor receptor
 CC alpha (GDNFRalpha).

Query Match 100.0%; Score 2488; DB 7; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDCLKEQSGCTKRTTLRQCVAGKETNF 60
 DB 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDCLKEQSGCTKRTTLRQCVAGKETNF 60
 QY 61 SLTSGLEAEDCSRAMEALKOKSLYNCRCRKGKKEKNCRLRIYWSYOSLQNDLLEDS 120
 DB 61 SLTSGLEAEDCSRAMEALKOKSLYNCRCRKGKKEKNCRLRIYWSYOSLQNDLLEDS 120
 QY 121 YEPVNSRLSDIFRAVPFISDFQVHEISKGNCLDAAKCNDLDTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFQVHEISKGNCLDAAKCNDLDTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRKKAKALRQFPDKVPKHSYGMALFCSGCDIACCTERRRQTIYVCSYEER 240
 DB 181 SMSNEVCNRRKKAKALRQFPDKVPKHSYGMALFCSGCDIACCTERRRQTIYVCSYEER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCKENYADCLAYSGLIGTWTPTN 300
 DB 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCKENYADCLAYSGLIGTWTPTN 300
 QY 301 YNDSSLSVAWPCDCNSGNDLDCLEKFLNPFKONTCLKNAIQAFNGSDVTWQAPAPV 360
 DB 301 YNDSSLSVAWPCDCNSGNDLDCLEKFLNPFKONTCLKNAIQAFNGSDVTWQAPAPV 360
 QY 361 OTTATTTTAFRYKKNPLGPAAGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSD 420
 DB 361 OTTATTTTAFRYKKNPLGPAAGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSD 420
 QY 421 GKDGGLAGASSHTTKSMAAPPSCSLSLPTMLTALALSVSLAETS 468
 DB 421 GKDGGLAGASSHTTKSMAAPPSCSLSLPTMLTALALSVSLAETS 468

RESULT 6
 ADE60800 standard; protein; 468 AA.
 AC ADE60800;
 XX 29-JAN-2004 (first entry)
 XX Rat Protein Q62997, SEQ ID NO 6712.
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS
 XX WO2003016475-A2.
 PN
 XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002MO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-033347P.
 XX (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'Urso D, Befort K, Costigan M,
 DR WPI; 2003-268312/26.
 DR GENBANK; Q62997.

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 468 AA;
 Query Match 100.0%; Score 2488; DB 7; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDCLKEQSGCTKRTTLRQCVAGKETNF 60
 DB 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDCLKEQSGCTKRTTLRQCVAGKETNF 60
 QY 61 SLTSGLEAEDCSRAMEALKOKSLYNCRCRKGKKEKNCRLRIYWSYOSLQNDLLEDS 120
 DB 61 SLTSGLEAEDCSRAMEALKOKSLYNCRCRKGKKEKNCRLRIYWSYOSLQNDLLEDS 120
 QY 121 YEPVNSRLSDIFRAVPFISDFQVHEISKGNCLDAAKCNDLDTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFQVHEISKGNCLDAAKCNDLDTCKKRSAYITPCTT 180

QY 181 SMSNEVCNRKCHALRQFPDKVPKAGSYGMLFCSGCRDIATERRRRTIIVPCSYEERER 240
 Db 181 SMSNEVCNRKCHALRQFPDKVPKAGSYGMLFCSGCRDIATERRRRTIIVPCSYEERER 240
 QY 241 PNCISLQDSCKTNYICRSRLADFFNNCOPESBSVSNCKENYADCLAYSGILGYMTPN 300
 Db 241 PNCISLQDSCKTNYICRSRLADFFNNCOPESBSVSNCKENYADCLAYSGILGYMTPN 300
 QY 301 YVDSLSLVAWPCDCNSGNDLEDCLKLFNFKNTCLKNAIQAFNGSDVYMMQAPAPV 360
 Db 301 YVDSLSLVAWPCDCNSGNDLEDCLKLFNFKNTCLKNAIQAFNGSDVYMMQAPAPV 360
 QY 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHYLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 Db 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHYLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 QY 421 GKDGLAGASHITTKSMAAPPSCSLSPVIMLTALALSVSLAETS 468
 Db 421 GKDGLAGASHITTKSMAAPPSCSLSPVIMLTALALSVSLAETS 468

RESULT 7

ID ADD46323 standard; protein, 468 AA.
 ADD46323;

29-JAN-2004 (first entry)

Rat Protein Q62997, SEQ ID NO 11998.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Rattus norvegicus.

W02003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP.

(FARB) BAYER AG.

Woolf C, D'Urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; Q62997.

New composition comprising two or more isolated polypeptides, useful for

preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat

or human polynucleotides or a polynucleotide which represents a fragment,

derivative or allelic variation of the nucleic acid sequence. Also

claimed are a vector comprising the novel polynucleotide, a host cell

comprising the vector, a method for identifying a nucleotide sequence

which is differentially regulated in an animal subjected to pain and a

kit to perform the method, an array, a method for identifying an agent

that increases or decreases the expression of the polynucleotide sequence

that is differentially expressed in neuronal tissue of a first animal

subjected to pain, a method for identifying a compound which regularly

the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a

compound that regulates the activity of one or more of the

polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPD at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 468 AA;

Query Match 100.0%; Score 2488; DB 7; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFIALTYFALPLDLMSAEVSGGRLDCVVASDQCKECSCTRYRTLRCVAGKETNF 60
 Db 1 MFIALTYFALPLDLMSAEVSGGRLDCVVASDQCKECSCTRYRTLRCVAGKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKQSLYNCRCKRGMKKNCLRIYMSYQSLQNDLLEDSF 120
 Db 61 SLTSGLEAKDCRSAMEALKQSLYNCRCKRGMKKNCLRIYMSYQSLQNDLLEDSF 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 Db 121 YEPVNSRLSDIFRAVPFISDFVQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRKCHALRQFPDKVPKAGSYGMLFCSGCRDIATERRRRTIIVPCSYEERER 240
 Db 181 SMSNEVCNRKCHALRQFPDKVPKAGSYGMLFCSGCRDIATERRRRTIIVPCSYEERER 240
 QY 241 PNCISLQDSCKTNYICRSRLADFFNNCOPESBSVSNCKENYADCLAYSGILGYMTPN 300
 Db 241 PNCISLQDSCKTNYICRSRLADFFNNCOPESBSVSNCKENYADCLAYSGILGYMTPN 300
 QY 301 YVDSLSLVAWPCDCNSGNDLEDCLKLFNFKNTCLKNAIQAFNGSDVYMMQAPAPV 360
 Db 301 YVDSLSLVAWPCDCNSGNDLEDCLKLFNFKNTCLKNAIQAFNGSDVYMMQAPAPV 360
 QY 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHYLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 Db 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHYLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 QY 421 GKDGLAGASHITTKSMAAPPSCSLSPVIMLTALALSVSLAETS 468
 Db 421 GKDGLAGASHITTKSMAAPPSCSLSPVIMLTALALSVSLAETS 468

RESULT 8

ADJ58694 standard; protein, 468 AA.

ADJ58694;

06-MAY-2004 (first entry)

Rat rectal protein.

Tissue growth; rect. protein; organ failure; foetal malformation;

tumour growth; renal tissue; cytostatic; vulnerary; nephroretropic; rat.

Rattus sp.

US6677135-B1.

13-JAN-2004.

06-NOV-1998; 98US-00187906.

XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 XX (BIOI) BIOGEN INC.
 XX Sanicola-Nadel M, Hession C, Cate RU, Worley DS;
 PI WPI: 2004-079845/08.
 XX N-PSDB; ADJ58653.
 DR
 XX New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
 PT treating diseases or conditions associated with aberrant expression or
 PT activity of the Ret ligand, such as organ failure, fetal malformations
 PT and tumor growth.
 CC
 PS Disclosure; SEQ ID NO 2; 66pp; English.
 XX
 CC The present invention relates to nucleotide and amino acid sequences
 CC which promote tissue growth and methods for modulating tissue growth. The
 CC invention also relates to ret proteins and polynucleotides encoding such
 CC proteins. Ret proteins interact with a receptor protein Ret to trigger
 CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
 CC the receptor protein Ret. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of diseases or
 CC conditions associated with aberrant expression and/or activity of the Ret
 CC ligand, such as organ failure, foetal malformations and tumour growth and
 CC for promoting regeneration or survival of damaged renal tissue. The
 CC present sequence is rat ret protein of the invention.
 CC
 SQ Sequence 468 AA;
 Query Match 100.0%; Score 2488; DB 8; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFATATYFALPLDLIMSAGVSGDRLDVCVAKSDOCLKEOSCTKYRTLRQCVAGKETNF 60
 DB 1 MFATATYFALPLDLIMSAGVSGDRLDVCVAKSDOCLKEOSCTKYRTLRQCVAGKETNF 60
 QY 61 SLTSGLEADECBSAMEALKOKSLVNCRCRKGKKKCNCLRIYMSYOSLGNDLLEDSP 120
 DB 61 SLTSGLEADECBSAMEALKOKSLVNCRCRKGKKKCNCLRIYMSYOSLGNDLLEDSP 120
 QY 61 SLTSGLEADECBSAMEALKOKSLVNCRCRKGKKKCNCLRIYMSYOSLGNDLLEDSP 120
 DB 61 SLTSGLEADECBSAMEALKOKSLVNCRCRKGKKKCNCLRIYMSYOSLGNDLLEDSP 120
 QY 121 YEPVNSRLSDIFRAVFPISDVFOQVEHISKGNCCDAAKACNLDPTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVFPISDVFOQVEHISKGNCCDAAKACNLDPTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRKCHKALRQFPDKVPAKSYGMLFCSCRDIACTERRRQTIIVPCSYEERER 240
 DB 181 SMSNEVCNRRKCHKALRQFPDKVPAKSYGMLFCSCRDIACTERRRQTIIVPCSYEERER 240
 QY 241 PNCLSLQSDCKTNYICRSRLADFTNCOPESSVSNCLKENYADCLLAYSGLIGYWTN 300
 DB 241 PNCLSLQSDCKTNYICRSRLADFTNCOPESSVSNCLKENYADCLLAYSGLIGYWTN 300
 QY 301 YNDSSLSLAPWDCNSGNDLEDCLKFLNFPKONTCLKAIAFNGSGSVTMMOPAPPY 360
 DB 301 YNDSSLSLAPWDCNSGNDLEDCLKFLNFPKONTCLKAIAFNGSGSVTMMOPAPPY 360
 QY 361 OTTATTTTAFRYKNPPLGPAENSEIPTHVLPPCANLQAKLSNVSGSTHCLSDSP 420
 DB 361 OTTATTTTAFRYKNPPLGPAENSEIPTHVLPPCANLQAKLSNVSGSTHCLSDSP 420
 QY 421 GKDGLAGASHITTKSMAAPSCSLSLPLVLMLTALAALLSVLAETS 468
 DB 421 GKDGLAGASHITTKSMAAPSCSLSLPLVLMLTALAALLSVLAETS 468

RESULT 9
 AAM92298
 ID AAM92298 standard; protein; 468 AA.
 XX
 AC AAM92298;
 XX
 DT 07-JUN-1999 (first entry)
 XX
 DE Rat GDNFR-alpha polypeptide.
 XX
 KM Glial Cell Line-Derived Neurotrophic Factor; GDNF; GDNF receptor; GDNFR;
 KM tyrosine phosphorylation; motoneuronal; neurodegenerative; human; rat;
 KM Parkinson's disease; GDNFR-beta; GDNFR-alpha.
 XX
 OS Rattus sp.
 XX
 PN M09852591-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 04-MAY-1998; 98WO-US009056.
 XX
 PR 22-MAY-1997; 97US-00861990.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Ibanez CF, Arumae U, Sariola H, Suvanto P, Trupp M, Saarna M;
 XX WPI: 1999-070126/06.
 DR
 XX Newly isolated and characterised GDNFR - used to further understand its
 PT biological action and the signalling events that occur when GDNFs bind to
 PT responsive cells.
 PT
 PS Disclosure; Fig 26A; 113pp; English.
 XX
 CC The invention relates to isolated Glial Cell Line-Derived Neurotrophic
 CC Factor Receptor (GDNFR) polypeptides. Isolated nucleic acid sequences
 CC encoding rat and human GDNFR-beta polypeptides are disclosed. GDNFR can
 CC be used in methods of identifying and isolating receptors. They can also
 CC be used for determining compounds/compositions that bind GDNF receptors.
 CC Similarly, the receptor is used to identify GDNF homologues by screening
 CC compounds/compositions exhibiting similar biological effects including
 CC tyrosine phosphorylation, and increases in c-fos mRNA and cell survival.
 CC GDNF analogues can be identified by screening compounds/compositions,
 CC which are antagonistic for the above biological effects. GDNF may have
 CC potential therapeutic use against motoneuronal and neurodegenerative
 CC diseases, especially Parkinson's disease. The isolation and
 CC characterisation of GDNF receptors will enable better understanding of
 CC its biological actions and the signalling events occurring when GDNF
 CC binds to responsive cells, which had previously been hindered by the lack
 CC of cell lines comprising GDNF receptors. The present sequence represents
 CC a rat GDNFR-alpha polypeptide
 CC
 SQ Sequence 468 AA;
 Query Match 99.4%; Score 2472; DB 2; Length 468;
 Best Local Similarity 99.6%; Pred. No. 9,6e-198;
 Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFATATYFALPLDLIMSAGVSGDRLDVCVAKSDOCLKEOSCTKYRTLRQCVAGKETNF 60
 DB 1 MFATATYFALPLDLIMSAGVSGDRLDVCVAKSDOCLKEOSCTKYRTLRQCVAGKETNF 60
 QY 61 SLTSGLEADECBSAMEALKOKSLVNCRCRKGKKKCNCLRIYMSYOSLGNDLLEDSP 120
 DB 61 SLTSGLEADECBSAMEALKOKSLVNCRCRKGKKKCNCLRIYMSYOSLGNDLLEDSP 120
 QY 121 YEPVNSRLSDIFRAVFPISDVFOQVEHISKGNCCDAAKACNLDPTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVFPISDVFOQVEHISKGNCCDAAKACNLDPTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRKCHKALRQFPDKVPAKSYGMLFCSCRDIACTERRRQTIIVPCSYEERER 240

Db 181 SMSNEVCNRRCKHCHALRQFFDKVPKHSYGMVFCSCBIDACTERRRQTIIVPCSYEBER 240
 QY 241 PNCISLDQSCNTNYICSRRLADFFNQCOPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
 Db 241 PNCISLDQSCNTNYICSRRLADFFNQCOPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
 QY 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 Db 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 QY 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANLQAQKLSKNSGTHLCLSDSD 420
 Db 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANLQAQKLSKNSGTHLCLSDSD 420
 QY 421 GKDGLAGASHITTKSMAPPSCSLSLPVLMTLAALLSVLAETS 468
 Db 421 GKDGLAGASHITTKSMAPPSCSLSLPVLMTLAALLSVLAETS 468

RESULT 10

AAM35333 standard; protein; 465 AA.
 AAM35333;
 01-MAY-1998 (first entry)

Human glial cell line-derived neurotrophic factor receptor.

Human, glial cell line-derived neurotrophic factor; GDNF; receptor;
 treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 gene therapy.

Homo sapiens.

MO9740152-A1.

30-OCT-1997.

15-APR-1997; 97WO-US006281.

22-APR-1996; 96US-0015907P.

09-MAY-1996; 96US-0017221P.

14-APR-1997; 97US-00837199.

(AMGE-) AMGEN INC.

Fox GM, Wen D, Jing S;

WPI; 1997-535836/49.

N-PSDB; AAT88419.

Glial cell line derived neurotrophic factor receptor - useful to treat

dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's

disease.

Claim 1; Page 91-93; 196pp; English.

The present sequence is the human glial cell line-derived neurotrophic
 factor (GDNF) receptor, which can be used to treat dopaminergic nerve
 cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic
 lateral sclerosis, complications of diabetes and Huntington's disease and
 hearing loss caused by injury to inner ear sensory neurons. The receptor
 can also be used to block unwanted GDNF activity, analyse GDNF related
 molecules and stabilise GDNF in pharmaceutical formulations. Receptor
 expressing cells, preferably transfected ex vivo, can be used similarly
 by implantation, and the use of the receptor cDNA in gene therapy is also
 contemplated. Probes based on the cDNA can be used to identify GDNF
 responsive cells and tissues, e.g. to identify patients who would benefit

CC from GDNF therapy, and abnormalities in receptor expression, and to
 CC isolate molecules that form a complex with the cDNA or are
 CC homologous/cross-reactive with the cDNA. Anti-receptor antibodies.
 CC oligonucleotides derived from the cDNA and animal models that overexpress
 CC the receptor can be used to study the biological function of GDNF.
 CC knockout transgenic animals can be used to detect GDNF dependent neurons
 CC or processes and the antibody can be used in immunoassays for the
 CC receptor. The receptor binds GDNF specifically and with high affinity,
 CC acting as part of a complex that mediates/enhances signal transduction by
 CC GDNF, i.e. increasing dopamine uptake in dopaminergic cells

Sequence 465 AA;

Query Match 93.1%; Score 2316.5; DB 2; Length 465;
 Best Local Similarity 92.7%; Pred. No. 9.6e-185;
 Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 MFATLYPALPLDLMSABVSGDRLDCVNASDQCKECSCTKYRTLRQVAGKETNF 60
 Db 1 MFATLYPALPLDLMSABVSGDRLDCVNASDQCKECSCTKYRTLRQVAGKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRGMKKRNCRIYWSWQSLQGNLLEDSP 120
 Db 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRGMKKRNCRIYWSWQSLQGNLLEDSP 120
 QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 Db 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHCHALRQFFDKVPKHSYGMVFCSCBIDACTERRRQTIIVPCSYEBER 240
 Db 181 SMSNEVCNRRCKHCHALRQFFDKVPKHSYGMVFCSCBIDACTERRRQTIIVPCSYEBER 240
 QY 241 PNCISLDQSCNTNYICSRRLADFFNQCOPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
 Db 241 PNCISLDQSCNTNYICSRRLADFFNQCOPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
 QY 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 Db 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 QY 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANLQAQKLSKNSGTHLCLSDSD 420
 Db 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANLQAQKLSKNSGTHLCLSDSD 420
 QY 421 GKDGLAGASHITTKSMAPPSCSLSLPVLMTLAALLSVLAETS 468
 Db 421 GKDGLAGASHITTKSMAPPSCSLSLPVLMTLAALLSVLAETS 468

RESULT 11

AAM84163 standard; protein; 465 AA.

AAM84163;

25-MAR-1999 (first entry)

Glial cell-line derived neurotrophic factor receptor-alpha cDNA.

Human, glial cell-line derived neurotrophic factor receptor-alpha;

GDNF-alpha; glial cell line-derived neurotrophic factor; GDNF;

neuturin; signal transduction; dopaminergic nerve cell;

Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;

neurological disorder; diabetes; glaucoma; sensory neuron;

retinal ganglion cell degeneration; sensory neuropathy; retinopathy;

gene therapy.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..18

/note="putative signal peptide"

FT Binding-site 18 /note= "may be involved in binding GDNF"
 FT Region 447..465
 FT /note= "hydrophobic region which may be involved in a
 FT glycosyl-phosphatidylinositol (GPI) anchorage of the
 FT receptor to the cytoplasmic membrane"
 XX
 PN MO9854213-A2.
 XX
 PD 03-DEC-1998.
 XX
 PF 27-APR-1998; 98MO-US008486.
 XX
 PR 30-MAY-1997; 97US-00866354.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Fox GM, Jing S, Wen D;
 XX
 DR MPI, 1999-080806/07.
 XX
 DR N-PSDB; AAV9310.
 XX
 XX New isolated glial cell line-derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. improperly functioning dopaminergic
 PT nerve cells; Parkinson's disease, Alzheimer's disease or amyotrophic
 PT lateral sclerosis.
 XX
 Claim 1; Fig 1A-M; 318pp; English.
 XX
 XX The present sequence represents a human glial cell-line derived
 CC neurotrophic factor receptor-alpha (GDNFR-alpha). The protein is capable
 CC of complexing with glial cell line-derived neurotrophic factor (GDNF) and
 CC mediating cell response to GDNF. GDNFR-alpha proteins are functionally
 CC characterized by the ability to bind GDNF and/or neurturin specifically,
 CC and to act as part of a molecular complex which mediates or enhances the
 CC signal transduction affects of GDNF and/or neurturin. The proteins can be
 CC used for treating improperly functioning dopaminergic nerve cells,
 CC Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons.
 CC pathological conditions, or disease or injury-related retinopathies. The
 CC products can also be used for detection, diagnosis, drug screening and
 CC gene therapy
 CC
 CC Sequence 465 AA:
 SQ
 Query Match 93.1%; Score 2316.5; DB 2; Length 465;
 Best Local Similarity 92.7%; Pred. No. 9.6e-185;
 Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

DB 301 YIDSSSLVAPWCDGNSGNDLEDCLEKFLNFFKONTCLKNAIQAFNGSDVTMMQAPPV 360
 QY 361 QTTATTTTAAFRVKNKPLGPGASENEIPHTVLPCCANLQAKXSNVSGSTHLCLSDSPF 420
 DB 361 QTTATTTTAAFRVKNKPLGPGASENEIPHTVLPCCANLQAKXSNVSGSTHLCLSDSPF 420
 QY 421 GKDLGAGSHITTKMAAPPCSLSLPYMLTALALISVLAETS 468
 DB 421 EKEGL-GASSHITTKMAAPPCSLSLPYMLTALALISVLAETS 465
 RESULT 12
 AB05547
 ID AB05547 standard; protein; 465 AA.
 XX
 AC AB05547;
 XX
 XX 14-NOV-2002 (first entry)
 DT
 DE Breast cancer-associated protein 12.
 XX
 KM Breast cancer; breast cancer-associated gene sequence; drug development;
 KM pharmacogenetics; biosensor development.
 XX
 OS Unidentified.
 XX
 PN MO200259377-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002MO-US002242.
 XX
 PR 24-JAN-2001; 2001US-0263965P.
 XX
 PR 02-FEB-2001; 2001US-0265928P.
 PR 09-APR-2001; 2001US-00829472.
 PR 09-APR-2001; 2001US-0282598P.
 PR 04-MAY-2001; 2001US-028590P.
 PR 29-MAY-2001; 2001US-0294443P.
 XX
 PA (EOS-) EOS BIOTECHNOLOGY INC.
 XX
 PI Mack DH, Gish KC, Afar D;
 XX
 XX MPI; 2002-583738/62.
 DR
 DR N-PSDB; ABT07704.
 XX
 PT Detecting a breast cancer-associated transcript in a patient's cell,
 PT useful for diagnosing breast cancer, comprises contacting a biological
 PT sample with a polynucleotide that selectively hybridizes with breast
 PT cancer nucleic acids.
 XX
 PS Disclosure; Page 357; 414pp; English.
 XX
 CC The invention comprises a method of detecting a breast cancer-associated
 CC transcript in a cell from a patient. The method of the invention involves
 CC contacting a biological sample from the patient with a nucleotide that
 CC hybridizes to one of the 69 breast cancer-associated gene sequences shown
 CC in the specification. The method of the invention is useful in the
 CC diagnosis or prognosis of breast cancer, and for detecting genes that are
 CC up or down-regulated in breast cancer cells. Genes identified by the
 CC method of the invention can be used in diagnostic purposes and also as
 CC targets for screening for therapeutic compounds that modulate breast
 CC cancer (e.g. hormones or antibodies). Identification of genes that are
 CC over or under expressed in breast cancer can additionally provide high-
 CC resolution, high-sensitivity datasets which can be used in the areas of
 CC diagnostics, therapeutics, drug development, pharmacogenetics, protein
 CC structure and biosensor development. Amino acid sequences AB05536 -
 CC AB05604 represent the proteins encoded by the 69 breast cancer-
 CC associated genes of the invention
 CC
 CC Sequence 465 AA:
 SQ

Query Match 93.1%; Score 2316.5; DB 5; Length 465;
 Best Local Similarity 92.7%; Pred. No. 9,6e-185;
 Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

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QY 1 MFATLYPALPLDLLMSAEVSGGDRLDVVASDQCLKEGSCSTYKRYTLRQCVAGKETNF 60
DB 1 MFATLYPALPLDLLMSAEVSGGDRLDVVASDQCLKEGSCSTYKRYTLRQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKKKSLYNCRCKGKKKKKCLRIYWSMTOSLGNDLLEDSF 120
DB 61 SLTSGLEAKDCRSAMEALKKKSLYNCRCKGKKKKKCLRIYWSMTOSLGNDLLEDSF 120
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI SKGNCCDAKACNLDDTCKKYSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCCDAKACNLDDTCKKYSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCCDAKACNLDDTCKKYSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCCDAKACNLDDTCKKYSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLRFDPKVPKSHSYGMLFCSCRDIACTERRRQTIYVCSYEBER 240
DB 181 SMSNEVCNRRCKHAKLRFDPKVPKSHSYGMLFCSCRDIACTERRRQTIYVCSYEBER 240
QY 241 PNCISLQDSCKNTYICRSRLADFFTNCPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
DB 241 PNCISLQDSCKNTYICRSRLADFFTNCPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
QY 301 YVDSSLSVAPWCDCSNGNDLEDCLEKFNFKNTCLKNAIQAFGNGSDVTMMQPAFV 360
DB 301 YVDSSLSVAPWCDCSNGNDLEDCLEKFNFKNTCLKNAIQAFGNGSDVTMMQPAFV 360
QY 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANLQAOKLSNVSGSTHCLSDSDF 420
DB 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANLQAOKLSNVSGSTHCLSDSDF 420
QY 421 GKGGLAGSSHTTKSMAPPSCSLSPVLMTLAALLSVSLAETS 468
DB 421 EKSGL-GASSHTTKSMAPPSCSLSPVLMTLAALLSVSLAETS 465

```

RESULT 13
 ADD11673
 ID ADD11673 standard; protein; 465 AA.

```

XX AC ADD11673;
XX DT 01-JAN-2004 (first entry)
XX DE Human glial cell line derived factor receptor alpha.
XX KW Human; Neurturin receptor alpha; NTNralpha; receptor; antiparkinsonian;
XX KW neurotrophic; neuroprotective; antidiabetic; cytokine; neurotrophic factor;
XX KW gene therapy; amyotrophic lateral sclerosis; diabetes;
XX KW Parkinson's disease; Alzheimer's disease;
XX KW glial cell line derived factor receptor alpha; GDNFralpha.
XX OS Homo sapiens.
XX PN US2003110525-A1.
XX PD 12-JUN-2003.
XX PF 03-FEB-2003; 2003US-00357822.
XX PR 18-FEB-1997; 97US-0038839P.
XX PR 09-JUN-1997; 97US-0049818P.
XX PR 24-OCT-1997; 97US-0063258P.
XX PR 17-FEB-1998; 98US-0002466S.
XX PR 01-SEP-1999; 99US-00388316.
XX PA (KLEI/) KLEIN R D.
XX PA (ROSE/) ROSENTHAL A.
XX PA (HYNE/) HYNES M A.
XX PI Klein RD, Rosenthal A, Hynes MA;

```

DR WPI; 2003-810859/76.
 XX New human neurturin receptor-alpha polypeptide useful for identifying a
 PT compound that binds to or activates it, potentially useful as a
 PT therapeutic.
 PS Example 1; SEQ ID NO 22; 83pp; English.

The invention relates to a polypeptide comprising a sequence that is a human neurturin receptor (NTNR) alpha extracellular domain or an allelic variant or mammalian homologue of NTNralpha. Also include are an antibody that specifically binds to NTNralpha, an isolated nucleic acid encoding NTNralpha, an expression vector comprising the nucleic acid, a host cell comprising the vector and a non-human transgenic animal which contains cells that express the nucleic acid to produce NTNralpha (or which contains cells having an altered NTNralpha gene). The NTNralpha protein may comprise mature NTNralpha conjugated with or fused to, a molecule which increases its serum half-life (e.g. IgG Fc or an IgG salvage receptor binding epitope). NTNralpha is used to identify a molecule which binds to or activates it, to purify a molecule which binds to it and to modulate a physiological response of a cell to neurturin. Soluble NTNralpha or soluble glial cell line derived factor alpha (GDNFralpha) is used for activating Ret on the surface of a cell. An antibody that binds to NTNralpha is used in a composition that further comprises a cytokine or a neurotrophic factor. The antibody is also used to determine the presence of NTNralpha in a test sample. An agonist antibody to NTNralpha is used for activating NTNralpha in a cell. A nucleic acid encoding NTNralpha is used to produce NTNralpha by culturing a host cell and recovering NTNralpha. A nucleic acid that encodes NTNralpha or antisense nucleic acid that inhibits expression of NTNralpha can be used in gene therapy. Examples of diseases that can be treated are amyotrophic lateral sclerosis, diabetes, Parkinson's disease, and Alzheimer's disease. The present sequence represents human glial cell line derived factor receptor alpha (GDNFralpha).

XX Sequence 465 AA;

Query Match 93.1%; Score 2316.5; DB 7; Length 465;
 Best Local Similarity 92.7%; Pred. No. 9,6e-185;
 Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

```

QY 1 MFATLYPALPLDLLMSAEVSGGDRLDVVASDQCLKEGSCSTYKRYTLRQCVAGKETNF 60
DB 1 MFATLYPALPLDLLMSAEVSGGDRLDVVASDQCLKEGSCSTYKRYTLRQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKKKSLYNCRCKGKKKKKCLRIYWSMTOSLGNDLLEDSF 120
DB 61 SLTSGLEAKDCRSAMEALKKKSLYNCRCKGKKKKKCLRIYWSMTOSLGNDLLEDSF 120
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI SKGNCCDAKACNLDDTCKKYSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCCDAKACNLDDTCKKYSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCCDAKACNLDDTCKKYSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHI PKGNCCDAKACNLDDTCKKYSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLRFDPKVPKSHSYGMLFCSCRDIACTERRRQTIYVCSYEBER 240
DB 181 SMSNEVCNRRCKHAKLRFDPKVPKSHSYGMLFCSCRDIACTERRRQTIYVCSYEBER 240
QY 241 PNCISLQDSCKNTYICRSRLADFFTNCPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
DB 241 PNCISLQDSCKNTYICRSRLADFFTNCPESRSVSNCLKENYADCLAYSGLIGVTWTPN 300
QY 301 YVDSSLSVAPWCDCSNGNDLEDCLEKFNFKNTCLKNAIQAFGNGSDVTMMQPAFV 360
DB 301 YVDSSLSVAPWCDCSNGNDLEDCLEKFNFKNTCLKNAIQAFGNGSDVTMMQPAFV 360
QY 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANLQAOKLSNVSGSTHCLSDSDF 420
DB 361 QTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPCCANLQAOKLSNVSGSTHCLSDSDF 420
QY 421 GKGGLAGSSHTTKSMAPPSCSLSPVLMTLAALLSVSLAETS 468
DB 421 EKSGL-GASSHTTKSMAPPSCSLSPVLMTLAALLSVSLAETS 465

```

RESULT 14
ADD46325 standard; protein; 465 AA.
AC ADD46325;
DT 29-JAN-2004 (first entry)
DE Human Protein P56159, SEQ ID NO 12000.
XX
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-268312/26.
XX DR GENBANK; P56159.
XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX PS Claim 1, Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIGO at
XX ftp.wigo.int/pub/published_pct_sequences.
XX
XX Sequence 465 AA;

Query Match 93.1%; Score 2316.5; DB 7; Length 465;
Best Local Similarity 92.7%; Pred. No. 9, 6e-185;
Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 MFLATLYPALPLDILMSAEVSGDRLDCVKASDQCLKEQSGSTKRTTLRQCVAKKETNF 60
DB 1 MFLATLYPALPLDILMSAEVSGDRLDCVKASDQCLKEQSGSTKRTTLRQCVAKKETNF 60
QY 61 SLTSGLEARDCEKSAEALKQSLVNCRCRCKGKKERKCLRIYMSYQSLQGNLLEDSF 120
DB 61 SLTSGLEARDCEKSAEALKQSLVNCRCRCKGKKERKCLRIYMSYQSLQGNLLEDSF 120
QY 121 YEPVNSRLSDIFRAVPFISDVFEQVVEHISKNNCLDAKACNLDPPCKKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFEQVVEHISKNNCLDAKACNLDPPCKKYRSAYITPCTT 180
QY 181 SMSNEVCNRRCKKALRQFPDKVPAHSGYGMIFCSGRDIACERRRQTIYPVCSYEBERER 240
DB 181 SVSNDVCNRRCKKALRQFPDKVPAHSGYGMIFCSGRDIACERRRQTIYPVCSYEBERER 240
QY 241 PNLCLSLQDSCKTMYICRSRLADFTNCOBESRSVSCLKENYADCLLAISGLIGTWTPN 300
DB 241 PNLCLSLQDSCKTMYICRSRLADFTNCOBESRSVSCLKENYADCLLAISGLIGTWTPN 300
QY 301 YVDSSSLVAWPCDCNSGNDLEDCLKFLNFKDNTCLKNALQAFGNGSDVTWMOAPAPV 360
DB 301 YVDSSSLVAWPCDCNSGNDLEDCLKFLNFKDNTCLKNALQAFGNGSDVTWMOAPAPV 360
QY 361 QTTTATTTTAFRVKNKPLCPAGSENEIPTHVLPPCANLQAKLKSXVSGSTHCLSDSDF 420
DB 361 QTTTATTTTAFRVKNKPLCPAGSENEIPTHVLPPCANLQAKLKSXVSGSTHCLSDSDF 420
QY 421 GRDGLAGASSHTTTRKMAAPSCSLSLPVMLTALALSVLAETS 468
DB 421 EKEGL-GASSHTTTRKMAAPSCSLSLPVLVLVLTALSTLL-SLTETS 465
RESULT 15
ADE60802 standard; protein; 465 AA.
ID ADE60802;
AC ADE60802;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human Protein P56159, SEQ ID NO 6714.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX
XX OS Homo sapiens.
XX
XX PN WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
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XX PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-268312/26.
XX DR GENBANK; P56159.
XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rht
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 465 AA;

Query Match	93.1%	Score 2316.5	DB 7	Length 465
Best Local Similarity	92.7%	Ref. No. 9.6e-185		
Matches 434, Conservative	16	Mismatches 13	Indels 3	Gaps 2

Qy	1	MEIATLYFALPLDILMSAEVSGSBDLDCYKASDOCLKEOSGSKTKRTLLQCAAGKETNF	60
Db	1	MEIATLYFALPLDILMSAEVSGSBDLDCYKASDOCLKEOSGSKTKRTLLQCAAGKETNF	60
Qy	61	SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKEKNCURIIYMSWYOSIQGNDLLEDSP	120
Db	61	SLASGLEAKDECRSAMEALKOKSLYNCRCKRGMKEKNCURIIYMSWYOSIQGNDLLEDSP	120
Qy	121	YEPVNSRLSDIRAVPFISDVPOOVHEIISKGNCCLDAAKCNLDITCKTKRSAYITPCTT	180
Db	121	YEPVNSRLSDIRAVPFISDVPOOVHEIIPGNNCLDAAKCNLDITCKTKRSAYITPCTT	180
Qy	181	SMSNSVCNRKCKCHKALROFFDKYPAKHSYGMLEFCSCRDIACTERRRQTIYPVCSYEERER	240
Db	181	SYSNVNVCNRKCKCHKALROFFDKYPAKHSYGMLEFCSCRDIACTERRRQTIYPVCSYEEREX	240
Qy	241	PNCGLSDOSCKTNYICRSRLADFTNCCOPESRSVSNCKENYADCLLAYSGLIGTWTPN	300
Db	241	PNCGLSDOSCKTNYICRSRLADFTNCCOPESRSVSNCKENYADCLLAYSGLIGTWTPN	300
Qy	301	YDSSSLSYAPMPCDCSGNSGNDLEDCIKFLNFPFNDNTCLKNAIQAFNGSGVYTWMPAPV	360
Db	301	YDSSSLSYAPMPCDCSGNSGNDLEDCIKFLNFPNDNTCLKNAIQAFNGSGVYTWMPAPV	360
Qy	361	QTTTATTTTAFVKNKPLCPAGSGENEIPTHVLPCCANLQAOXKLKSNVSGSTHLCLSDSDF	420
Db	361	QTTTATTTTALFVKNKPLCPAGSGENEIPTHVLPCCANLQAOXKLKSNVSGWTHLCSISGNY	420
Qy	421	GDDGLAGASHTTTKSMAPPGCSLSPLMLTALAALLSVLSAETS	468
Db	421	EEGGLGASHTTTKSMAPPGCSGLPLVLVYTAALSTLL-SLTERS	465

Search completed: February 17, 2005, 09:46:12
Job time : 85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:18 ; Search time 139 Seconds
(Without alignments)
1101.790 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488

Sequence: 1 MEIATVYFALPLDILMSAE.....PILMTALALSLVSLAERS 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 segs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2488	100.0	468	14	US-10-673-007-1
5	2316.5	93.1	465	14	US-10-357-822-22
6	2316.5	93.1	465	14	US-10-155-693-2
7	2316.5	93.1	465	14	US-10-295-027-84
8	2316.5	93.1	465	14	US-10-058-270A-24
9	2311.5	92.9	463	14	US-10-155-693-12
10	2310.5	92.9	465	16	US-10-673-007-8
11	2309.5	92.8	465	14	US-10-155-693-6
12	2306.5	92.7	463	14	US-10-155-693-10
13	2278	91.6	460	14	US-10-241-220-62

14	1431.5	57.5	294	14	US-10-155-693-16	Sequence 16, Appl
15	1220	49.0	232	14	US-10-155-693-14	Sequence 14, Appl
16	1120.5	45.0	464	4	US-09-388-316-6	Sequence 6, Appl1
17	1120.5	45.0	464	14	US-10-357-822-6	Sequence 6, Appl1
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19	1117.5	44.9	464	4	US-09-388-316-3	Sequence 3, Appl1
20	1117.5	44.9	464	14	US-10-357-822-3	Sequence 3, Appl1
21	1108.5	44.6	464	16	US-10-673-007-9	Sequence 9, Appl1
22	1100	44.2	664	9	US-09-388-316-18	Sequence 18, Appl
23	1100	44.2	664	14	US-10-357-822-18	Sequence 18, Appl
24	1099.5	44.2	664	14	US-09-388-316-16	Sequence 16, Appl
25	1099.5	44.2	664	14	US-10-357-822-16	Sequence 16, Appl
26	1098.5	44.2	445	16	US-10-673-007-11	Sequence 11, Appl
27	1035.5	41.6	219	14	US-10-155-693-18	Sequence 18, Appl
28	983.5	39.5	209	14	US-10-155-693-20	Sequence 20, Appl
29	946.5	26.0	147	14	US-10-155-693-22	Sequence 22, Appl
30	617.5	24.8	141	14	US-10-155-693-24	Sequence 24, Appl
31	573	23.0	120	9	US-09-864-761-47340	Sequence 47340, A
32	511	20.5	400	9	US-09-220-920-63	Sequence 63, Appl
33	511	20.5	400	9	US-09-828-366-16	Sequence 16, Appl
34	505.5	20.3	397	9	US-09-220-920-64	Sequence 64, Appl
35	227	9.1	132	10	US-09-866-050A-709	Sequence 709, App
36	214	8.6	394	15	US-10-369-904-2	Sequence 2, Appl1
37	148	5.9	3051	15	US-10-369-493-5866	Sequence 5866, Ap
38	136	5.5	207	9	US-09-893-737-160	Sequence 160, App
39	131	5.3	2471	15	US-10-190-115-27	Sequence 27, Appl
40	131	5.3	2471	15	US-10-369-072-27	Sequence 27, Appl
41	129	5.2	770	14	US-10-281-478-11	Sequence 11, Appl
42	123.5	5.0	2195	15	US-10-369-493-6828	Sequence 6828, Ap
43	122	4.9	2503	16	US-10-322-281-723	Sequence 723, App
44	121.5	4.9	886	9	US-09-992-647-11	Sequence 11, Appl
45	121.5	4.9	886	14	US-10-225-567A-50	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-10-033-350-2
; Sequence 2, Application US/10033350
; Publication No. US2003002284A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
Klein, Robert D.
Moore, Mark W.
Rosenthal, Arnon
Ryan, Anne M.
TITLE OF INVENTION: USES OF GDNF AND GDNF RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,350
FILING DATE: 02-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,370
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US97/04363
FILING DATE: 13-Mar-1997
APPLICATION NUMBER: 08/615902
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: 08/618236

	FILING DATE:	14-MAR-1996
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Torchia, Phd., Timothy E.
	REGISTRATION NUMBER:	36,700
	REFERENCE/DOCKET NUMBER:	P0996PICT
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	650/225-8674
	TELEFAX:	650/952-9881
	INFORMATION FOR SEQ ID NO:	2:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	468 amino acids
	TYPE:	Amino Acid
	TOPOLOGY:	Linear
	FEATURE:	
	NAME/KEY:	Extracellular Domain
	LOCATION:	25
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
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	NAME/KEY:	Mature Protein N-terminal
	LOCATION:	25-427
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
	FEATURE:	
	NAME/KEY:	Potential Glycosylation Site
	LOCATION:	349
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
	FEATURE:	
	NAME/KEY:	Potential Glycosylation Site
	LOCATION:	408
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
	FEATURE:	
	NAME/KEY:	Potential Glycosylation Site
	LOCATION:	61
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
/	SEQUENCE DESCRIPTION:	SEQ ID NO: 2:
/		
/		
US-10-033-350-2		
	Query Match	100.0%; Score 2489; DB 14; Length 468;
	Best Local Similarity	100.0%; Pred. No. 7.8e-210;
	Matches 468; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MFLLATLYPALPLDLLILMSAEVSGGRLDVCVKASDCLIKSQSSTGYRTLROCVAKETNF 60
DB	1	MFLLATLYPALPLDLLILMSAEVSGGRLDVCVKASDCLIKSQSSTGYRTLROCVAKETNF 60
QY	61	SLSGLSEKADBEGRSAMKALKKOKSLYNCRCKRMKEKNCLRIYWSMYOSLGNDLLEDSP 120
DB	61	SLSGLSEKADBEGRSAMKALKKOKSLYNCRCKRMKEKNCLRIYWSMYOSLGNDLLEDSP 120
QY	121	YEPVNSRLSDIFRAVPFTISDVFOQVEHISKGNCCIDAAACNLDDTCKXYSAYITPCTT 180
DB	121	YEPVNSRLSDIFRAVPFTISDVFOQVEHISKGNCCIDAAACNLDDTCKXYSAYITPCTT 180
QY	181	SMSNEVNCRRKCHKALROFPEDVPKHSYGMLFCSCRDIACTERRRQTIVPCSYEEER 240
DB	181	SMSNEVNCRRKCHKALROFPEDVPKHSYGMLFCSCRDIACTERRRQTIVPCSYEEER 240
QY	241	PNCULSDQSKTNVIICRSRLADFTNCCPEBSRVSNCLKENYADCLLAYSGLIGVTMTPN 300
DB	241	PNCULSDQSKTNVIICRSRLADFTNCCPEBSRVSNCLKENYADCLLAYSGLIGVTMTPN 300
QY	301	VVDSSSLVAAPWCDCSNSGNDLEDCLKFLNFKXONTCLKNAIQAFNGSDVTMMOPAPPV 360
DB	301	VVDSSSLVAAPWCDCSNSGNDLEDCLKFLNFKXONTCLKNAIQAFNGSDVTMMOPAPPV 360
QY	361	QTTATATTTAFFVKKPKLPAGASENEIPHHVLPCCANLQAQGLKSNAVSGSTHLCLSDSP 420
DB	361	QTTATATTTAFFVKKPKLPAGASENEIPHHVLPCCANLQAQGLKSNAVSGSTHLCLSDSP 420

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Oy      422  GKGGLAGASHITTKSMAAPFCSJSLSPVMTALAAALSVSLAETS 468
      |||||
Db      421  GKGGLAGASHITTKSMAAPFCSJSLSPVMTALAAALSVSLAETS 468

      RESULT 2
      US-10-357-822-21
      ; Sequence 21. Application US/10357822
      ; Publication No. US20030110525A1
      ; GENERAL INFORMATION:
      ; APPLICANT: KLEIN, ROBERT D.
      ; APPLICANT: ROSENTHAL, ARNON
      ; APPLICANT: HYNES, MARY A.
      ; TITLE OF INVENTION: NEUTRIN RECEPTOR
      ; FILE REFERENCE: GENENT. 45A2DVA
      ; CURRENT APPLICATION NUMBER: US/10/357, 822
      ; CURRENT FILING DATE: 2003-02-03
      ; PRIOR APPLICATION NUMBER: US/09/388, 316C
      ; PRIOR FILING DATE: 1999-09-01
      ; PRIOR APPLICATION NUMBER: 09/024, 665
      ; PRIOR FILING DATE: 1998-02-17
      ; PRIOR APPLICATION NUMBER: 60/063, 258
      ; PRIOR FILING DATE: 1997-10-24
      ; PRIOR APPLICATION NUMBER: 60/049, 818
      ; PRIOR FILING DATE: 1997-06-09
      ; PRIOR APPLICATION NUMBER: 60/038, 839
      ; PRIOR FILING DATE: 1997-02-18
      ; NUMBER OF SEQ ID NOS: 30
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 21
      ; LENGTH: 468
      ; TYPE: PRT
      ; ORGANISM: Ratticus norveticus
      ; US-10-357-822-21

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Query Match	Similarity	100.0%	Score 2488	DB 14	Length 468
Best Local	Similarity	100.0%	Pred. No. 7.8e-210		
Matches 468	Conservative	0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MFLATLYPALPLILDLMSAEVSGGDRLD	CVASADQCLKEQSCSTKYRTLRQCVAKETNF	60	
Db	1	MFLATLYPALPLILDLMSAEVSGGDRLD	CVASADQCLKEQSCSTKYRTLRQCVAKETNF	60	
Qy	61	SLTSGLEADECBSAMEALKOKSLYNPCCKRGKKEKNCIRIYMSYQSLQGNDLLEDS	120		
Db	61	SLTSGLEADECBSAMEALKOKSLYNPCCKRGKKEKNCIRIYMSYQSLQGNDLLEDS	120		
Qy	121	YEFVNSRLSDIFRAVPFISDVFOQYEHISKKNCLDLAAKCNLDPTCKYRSAYITPCT	180		
Db	121	YEFVNSRLSDIFRAVPFISDVFOQYEHISKKNCLDLAAKCNLDPTCKYRSAYITPCT	180		
Qy	181	SMSNEVCNRKCHKALROFPDKVPKASHYGMFPCSCRDIACTERRRQITVPVCSEBER	240		
Db	181	SMSNEVCNRKCHKALROFPDKVPKASHYGMFPCSCRDIACTERRRQITVPVCSEBER	240		
Qy	241	PNCLSLQDSCKNMYICRSRLADFPNOCPEBSRVSNCLEKNYADCLLAISGLIGTMTPN	300		
Db	241	PNCLSLQDSCKNMYICRSRLADFPNOCPEBSRVSNCLEKNYADCLLAISGLIGTMTPN	300		
Qy	301	YVDSSSLVAAPMCDSCNSGNDLEDCLEKLFNFKCNTCLKNAIQAFNGSGDVTMMQAPAPV	360		
Db	301	YVDSSSLVAAPMCDSCNSGNDLEDCLEKLFNFKCNTCLKNAIQAFNGSGDVTMMQAPAPV	360		
Qy	361	QTTTATTTTAAFRVKKRPIGPAGSENEIPTHYLPCCANLQOKLSNVSSGTHCLSDSPF	420		
Db	361	QTTTATTTTAAFRVKKRPIGPAGSENEIPTHYLPCCANLQOKLSNVSSGTHCLSDSPF	420		
Qy	421	GKQGLAGASSHTTKSMAAPSCSLSLPVLMTLALALSVSLAETS	468		
Db	421	GKQGLAGASSHTTKSMAAPSCSLSLPVLMTLALALSVSLAETS	468		

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US-10-155-693-4
; Sequence 4, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: MEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 468
; TYPE: PRT
; ORGANISM: RAT
US-10-155-693-4

Query Match      100.0%; Score 2488; DB 14; Length 468;
Best Local Similarity 100.0%; Pred. No. 7,8e-210;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKRTTLQCVAGKETNF 60
DB 1 MFPLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKRTTLQCVAGKETNF 60
QY 61 SLTSGLEADQECRSAMEALQKSLYNCRCKRGKKEKNCIRIYMSYQSLQGNLDLSDP 120
DB 61 SLTSGLEADQECRSAMEALQKSLYNCRCKRGKKEKNCIRIYMSYQSLQGNLDLSDP 120
QY 121 YEPVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDPTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCKHALRQFPDKVPAGHSYGMFLCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMSNEVCNRRKCKHALRQFPDKVPAGHSYGMFLCSCRDIACTERRRQTIYPVCSYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFFTNCOPEBSRSVSNCKENYADCLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFFTNCOPEBSRSVSNCKENYADCLAYSGLIGTWTPN 300
QY 301 YVDSSLSVAPWMDCSNGNDLEDCLEKFLNPFKONTCLKNAIOAFNGSDVTWMOAPAPV 360
DB 301 YVDSSLSVAPWMDCSNGNDLEDCLEKFLNPFKONTCLKNAIOAFNGSDVTWMOAPAPV 360
QY 361 QTTTATTTTAFRYKXNKPPLGAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSD 420
DB 361 QTTTATTTTAFRYKXNKPPLGAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSD 420
QY 421 GKQGLAGASSHITTKSMAAPPSCSLSLPYLMLTALAALLSVLAETS 468
DB 421 GKQGLAGASSHITTKSMAAPPSCSLSLPYLMLTALAALLSVLAETS 468

RESULT 4
US-10-673-007-1
; Sequence 1, Application US/10673007
; Publication No. US20040126819A1
; GENERAL INFORMATION:
; APPLICANT: Ibanez, Carlos F.
; APPLICANT: Artumae, Urmes
; APPLICANT: Sariola, Hannu
; APPLICANT: Suanto, Petro
; APPLICANT: Trupp, Miles
; APPLICANT: Saarna, Mart
```

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; TITLE OF INVENTION: Glial Cell Line-Derived Neurotropic Factor Receptors
; FILE REFERENCE: CEPH0418
; CURRENT APPLICATION NUMBER: US/10/673,007
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/08/861,990
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: 08/747,842
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: 60/006,619
; PRIOR FILING DATE: 1995-11-13
; PRIOR APPLICATION NUMBER: 60/015,767
; PRIOR FILING DATE: 1996-04-16
; PRIOR APPLICATION NUMBER: 60/021,965
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,638
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,639
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-673-007-1

Query Match      100.0%; Score 2488; DB 16; Length 468;
Best Local Similarity 100.0%; Pred. No. 7,8e-210;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKRTTLQCVAGKETNF 60
DB 1 MFPLATYFALPLDLMSAEVSGDRLDCVKASDQCKEOSTKRTTLQCVAGKETNF 60
QY 61 SLTSGLEADQECRSAMEALQKSLYNCRCKRGKKEKNCIRIYMSYQSLQGNLDLSDP 120
DB 61 SLTSGLEADQECRSAMEALQKSLYNCRCKRGKKEKNCIRIYMSYQSLQGNLDLSDP 120
QY 121 YEPVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDPTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCKHALRQFPDKVPAGHSYGMFLCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMSNEVCNRRKCKHALRQFPDKVPAGHSYGMFLCSCRDIACTERRRQTIYPVCSYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFFTNCOPEBSRSVSNCKENYADCLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFFTNCOPEBSRSVSNCKENYADCLAYSGLIGTWTPN 300
QY 301 YVDSSLSVAPWMDCSNGNDLEDCLEKFLNPFKONTCLKNAIOAFNGSDVTWMOAPAPV 360
DB 301 YVDSSLSVAPWMDCSNGNDLEDCLEKFLNPFKONTCLKNAIOAFNGSDVTWMOAPAPV 360
QY 361 QTTTATTTTAFRYKXNKPPLGAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSD 420
DB 361 QTTTATTTTAFRYKXNKPPLGAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSD 420
QY 421 GKQGLAGASSHITTKSMAAPPSCSLSLPYLMLTALAALLSVLAETS 468
DB 421 GKQGLAGASSHITTKSMAAPPSCSLSLPYLMLTALAALLSVLAETS 468

RESULT 5
US-10-357-822-22
; Sequence 22, Application US/10357822
; Publication No. US20030110525A1
; GENERAL INFORMATION:
; APPLICANT: KLEIN, ROBERT D.
; APPLICANT: ROSENTHAL, ARNON
; APPLICANT: HYNES, MARY A.
; TITLE OF INVENTION: NEURTURIN RECEPTOR
; FILE REFERENCE: GENENT, 45A2DV1
```

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CURRENT APPLICATION NUMBER: US/10/357, 822
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US/09/388, 316C
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: 09/024, 665
PRIOR FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 60/063, 258
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/049, 818
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: 60/038, 839
PRIOR FILING DATE: 1997-02-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
US-10-357-822-22

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	Query Match	Similarity	Score	216 5;	DB 14;	Length	465;
	Match	Local	Similarity	92.7%;	Pred.	No.9.1e-195;	
	Matches	434;	Conservative	18;	Indels	13;	Gaps
						3;	Gaps
							2
QY	1	MFATLYPALPLDLLLMSAEVSGGRDL	CVKASDCLKEQSCSTKYRILRQC	VAGKETNF	60		
Db	1	MFATLYPALPLDLLLMSAEVSGGRDL	CVKASDCLKEQSCSTKYRILRQC	VAGKETNF	60		
QY	61	SLTSGLEAKDECRS	AMEALKOKSLYNCRCKRMKKEKNC	LRIYMSYOSLQGNDDLEDSP	120		
Db	61	SLTSGLEAKDECRS	AMEALKOKSLYNCRCKRMKKEKNC	LRIYMSYOSLQGNDDLEDSP	120		
QY	121	YEPNRSRSDI	FRAVPFISDVFOQVEHISKNNCC	DLAAKACNLDPTCKKYRSAYITPCTT	180		
Db	121	YEPNRSRSDI	FRAVPFISDVFOQVEHISKNNCC	DLAAKACNLDPTCKKYRSAYITPCTT	180		
QY	181	SMSNEVCNRKCKHAKLRQ	FDKVPKAGSYGMLFCSCRD	IACERRRQTI	VPVCSYBERER	240	
Db	181	SMSNEVCNRKCKHAKLRQ	FDKVPKAGSYGMLFCSCRD	IACERRRQTI	VPVCSYBERER	240	
QY	241	PNCISLQDSC	KTNYSICRSRLADFP	FNCOPESSSVSNCKENYADCL	IAYSGIIGVTMTN	300	
Db	241	PNCISLQDSC	KTNYSICRSRLADFP	FNCOPESSSVSNCKENYADCL	IAYSGIIGVTMTN	300	
QY	301	YVDSSSLSVA	PMCDSCNSGNDLEDCLK	PLNFKDMTCLKNALQAFNGSD	VTMMQAPAPV	360	
Db	301	YVDSSSLSVA	PMCDSCNSGNDLEDCLK	PLNFKDMTCLKNALQAFNGSD	VTMMQAPAPV	360	
QY	361	QTTATTTAA	RVKNNKPLGPAGSENEI	PHVLP	PCANLQAO	KLKNVSGSTHCL	SDSDP
Db	361	QTTATTTAA	RVKNNKPLGPAGSENEI	PHVLP	PCANLQAO	KLKNVSGSTHCL	SDSDP
QY	421	GKQGLAGASS	HTTKSMAAPPSCSI	SSLSL	EVMLTALALLSV	SLAETS	468
Db	421	GKQGLAGASS	HTTKSMAAPPSCSI	SSLSL	EVMLTALALLSV	SLAETS	468

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1  PRIOR APPLICATION NUMBER: US 60/017,221
2  PRIOR FILING DATE: 1996-05-09
3  NUMBER OF SEQ ID NOS: 47
4  SOFTWARE: PatentIn version 3.1
5  SEQ ID NO 2
6  LENGTH: 465
7  TYPE: PR1
8  ORGANISM: HUMAN
9  FEATURE:
10 NAME/KEY: misc_feature
11 LOCATION: (2078)..(2078)
12 OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
13 FEATURE:
14 NAME/KEY: misc_feature
15 LOCATION: (2107)..(2107)
16 OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
17 FEATURE:
18 NAME/KEY: ferent_receptor_clones
19 LOCATION: (2241)..(2241)
20 OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
21 FEATURE:
22 NAME/KEY: ferent_receptor_clones
23 LOCATION: (2250)..(2250)
24 OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif
25 FEATURE:
26 NAME/KEY: ferent_receptor_clones
27 LOCATION: (2256)..(2256)
28 OTHER INFORMATION: N in position 2256 to 2294 indicates positions of divergence be
29 OTHER INFORMATION: tween different receptor clones
30 US-10-155-693-2

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Query Match	93.1%;	Score 2316.5;	DB 14;	Length 465;
Best Local Similarity	92.7%;	Pred. No. 9.1e-195;		
Matches 434;	Conservative 18;	Mismatches 13;	Indels 3;	Gaps 2

Qy	1	MFATLTFEALPLDLMLMSAEVSGSDRLDDCYKASPOCLKEGSGTKRTRLLRQCAVAGKNTFN	60
Db	1	MFATLTFEALPLDLMLMSAEVSGSDRLDDCYKASPOCLKEGSGTKRTRLLRQCAVAGKNTFN	60
Qy	61	SLTSGLEAKDECRSAMEALNQKSLYNCRCKRGKKEKNCRIYWSMYOSLQGNLLEDSP	120
Db	61	SLAGSLAKDECRSAMEALNQKSLYNCRCKRGKKEKNCRIYWSMYOSLQGNLLEDSP	120
Qy	121	YEPNRSRLSDIFRAVPIPSIDVFOQVEHISKGNCLDAAKCNLDPTCKKRSAYITPCTT	180
Db	121	YEPNRSRLSDIFRAVPIPSIDVFOQVEHISKGNCLDAAKCNLDPTCKKRSAYITPCTT	180
Qy	181	SMSNEVCNRRKCHKALQFDFKVPAAKSYGMFLFCSGCRDIACTERRRQTIIPVCSYEERER	240
Db	181	SVSNDDVCNRRKCHKALQFDFKVPAAKSYGMFLFCSGCRDIACTERRRQTIIPVCSYEERER	240
Qy	241	PNCISLDDSCCKNTYICRSRLADFFTNCCPESRSVSNCKENYADCLLANSGLIGIYWTEN	300
Db	241	PNCISLDDSCCKNTYICRSRLADFFTNCCPESRSVSNCKENYADCLLANSGLIGIYWTEN	300
Qy	301	YVDSLSLSVAPMPCDCSSGNDLDEPCLKEFLNFPFQDNTCLKNAIOAFGNGSDVYMMQAPVP	360
Db	301	YVDSLSLSVAPMPCDCSSGNDLDEPCLKEFLNFPFQDNTCLKNAIOAFGNGSDVYMMQAPVP	360
Qy	361	QTTATATTTTFRVKNKRLGPAGSENEIPTHTVLPCCANTQAOKLSKNVSGSTHLCLSDSP	420
Db	361	QTTATATTTTFRVKNKRLGPAGSENEIPTHTVLPCCANTQAOKLSKNVSGSTHLCLSDSP	420
Qy	421	GKQGLAGASHITTKSMAAPPCSCSLSPVLTMLTALAALLSVLAETS	468
Db	421	EKEBL-GASSHITTKSMAAPPCSCSLSPVLTMLTALAALLSVLAETS	465

RESULT 7


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US-10-295-027-84
: Sequence 84, Application US/10295027
: Publication No US20030232350A1
: GENERAL INFORMATION:
: APPLICANT: Afar, Daniel
: APPLICANT: Aziz, Natasha
: APPLICANT: Ginsberg, Wendy M.
: APPLICANT: Glah, Kurt C.
: APPLICANT: Glynn, Richard
: APPLICANT: Hevez, Peter A.
: APPLICANT: Mack, David H.
: APPLICANT: Murray, Richard
: APPLICANT: Watson, Susan R.
: APPLICANT: Eos Biotechnology, Inc.
: TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
: FILE REFERENCE: 018501-012500US
: CURRENT APPLICATION NUMBER: US/10/295,027
: CURRENT FILING DATE: 2002-11-13
: PRIOR APPLICATION NUMBER: US 09/663,733
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: US 60/350,666
: PRIOR FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/335,394
: PRIOR FILING DATE: 2001-11-15
: PRIOR APPLICATION NUMBER: US 60/332,464
: PRIOR FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: US 60/334,393
: PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US 60/340,376
: PRIOR FILING DATE: 2001-12-14
: PRIOR APPLICATION NUMBER: US 60/347,211
: PRIOR FILING DATE: 2002-01-08
: PRIOR APPLICATION NUMBER: US 60/347,349
: PRIOR FILING DATE: 2002-01-10
: PRIOR APPLICATION NUMBER: US 60/355,250
: PRIOR FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: US 60/356,714
: PRIOR FILING DATE: 2002-02-13
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 1386
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 84
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-295-027-84

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[illegible]

Db 301 YIDSSLSVAWPCDCSNGNDLBECKLFNFKDXTCLKMNAIQAFNGSDVTVWQAPFV 360

QY 361 OTTATTTTAAKVKKPLGPAKSENEIPTHVLPKCANIQAOQLKSNVSGSTHLCISDSE 420

Db 361 OTTATTTTAAKVKKPLGPAKSENEIPTHVLPKCANIQAOQLKSNVSGSTHLCISNGN 420

QY 421 GKDGLAGASSHITTKSMAAPSCSLSPLVIMLTALAILSVLAETS 468

Db 421 EKEGL-GASSHITTKSMAAPSCGSLPLVLVTVTASLTLL--SLRETS 465

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RESULT 8
US-10-058-270A-24
; Sequence 24, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058, 270A
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 465
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-058-270A-24

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Query Match	Similarity	93.1%	Score 2316.5	DB 15	Length 465
Best Local	Similarity	92.7% <td>Pred. No. 9.1e-195</td> <td></td> <td></td>	Pred. No. 9.1e-195		
Matches	434	Conservative	18	Mismatches	13
				Indels	3
				Gaps	2

QY	DB	1	MFATLYPALPLDLLMSAEVSGGDRDLCCVKASDCLKEQSCSTYRTLROCVAKETNF	60
QY	DB	61	SLTSLLEAKDCRSAMEALKOKSLYNCRCKRGMKKEKXCLRIYMSYOSLOQNDLLEDSP	120
QY	DB	61	SLASLEAKDECRSAMEALKOKSLYNCRCKRGMKKEKXCLRIYMSYOSLOQNDLLEDSP	120
QY	DB	121	YEPVNSRLSDIFRAVPFIISDVAPQVQVEHISKGNCCIDAAKACMLDPTCKKYSAYITPCTT	180
QY	DB	121	YEPVNSRLSDIFRAVPFIISDVAPQVQVEHISKGNCCIDAAKACMLDPTCKKYSAYITPCTT	180
QY	DB	181	SMSNEVNCRRKCHKALROFPDVKVPAKHSYGMFLFCSCRDICTACERRRQTIYVPCSYEERER	240
QY	DB	181	SVSNDVNCRRKCHKALROFPDVKVPAKHSYGMFLFCSCRDICTACERRRQTIYVPCSYEERER	240
QY	DB	241	PNCISLADQSCKNTNYICRSRLADFTFNCPQPSRHSVSNCLKENYADCLLAYSGLIGVTMTN	300
QY	DB	241	PNCISLADQSCKNTNYICRSRLADFTFNCPQPSRHSVSNCLKENYADCLLAYSGLIGVTMTN	300
QY	DB	301	YVDSSSLVAAWPCDCSNGSNGDLEDCCLKLNFPKNDTCLKNALQAFNGSGDVTMMQAPPV	360
QY	DB	301	YIDSSSLVAAWPCDCSNGSNGDLEDCCLKLNFPEKNDTCLKNALQAFNGSGDVTMMQAPPV	360

QY 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSVSGSTHLCISDSDF 420
Db 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSVSGSTHLCISDSDF 420
QY 421 GKDLGAGASSHITTKSMAAPPSCGSLSLPLVMTALAILSVLAETS 468
Db 421 EKEGL-GASSHITTKSMAAPPSCGSLPLVLVMTALSTLL--SLTETS 465

RESULT 9

US-10-155-693-12
; Sequence 12, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 463
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(539)
; OTHER INFORMATION: No. US20030175876A1e="1 to 539 18 -237 to 301 of Figure 5 21bcon
US-10-155-693-12

Query Match 92.9%; Score 2311.5; DB 14; Length 463;

Best Local Similarity 92.9%; Pred. No. 2.5e-194;

Matches 430; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFATLTYFALPLDILMSAEVSGGRLDVCVKSDDCKECSCTKYRTLROCVAGKETNF 60
Db 1 MFATLTYFALPLDILMSAEVSGGRLDVCVKSDDCKECSCTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDEBCRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
Db 61 SLTSGLEAKDEBCRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
QY 121 YEPVNSRLSDTFRVVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
Db 121 YEPVNSRLSDTFRVVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCKHAKLROFPDVKVPAKHSYGMFLFCSCRDIACTERRRQTIIVPCSYEERER 240
Db 181 SVSNDVCCRCKHAKLROFPDVKVPAKHSYGMFLFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCNLSDSCSKTNYICRSLADFTFNCOPESRSVSNCLKENYADCLLAYSGLIGVTMTN 300
Db 241 PNCNLSDSCSKTNYICRSLADFTFNCOPESRSVSNCLKENYADCLLAYSGLIGVTMTN 300
QY 301 YVDSSSLVAPWCCDSNSGNDLEBCLKFNFKNTCLKNAIQAFGNSDVTVMQPAFPV 360
Db 301 YVDSSSLVAPWCCDSNSGNDLEBCLKFNFKNTCLKNAIQAFGNSDVTVMQPAFPV 360
QY 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSVSGSTHLCISDSDF 420
Db 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSVSGSTHLCISDSDF 420
QY 421 GKDLGAGASSHITTKSMAAPPSCGSLSLPLVMTALAILSVLAETS 468
Db 421 GKDLGAGASSHITTKSMAAPPSCGSLSLPLVMTALAILSVLAETS 468

Db 421 EKEGL-GASSHITTKSMAAPPSCGSLPLVLVMTALSTLLSLT 462

RESULT 10

US-10-673-007-8
; Sequence 8, Application US/10673007
; Publication No. US20040126819A1
; GENERAL INFORMATION:
; APPLICANT: Ibanez, Carlos F.
; APPLICANT: Arumae, Urmas
; APPLICANT: Saitola, Hannu
; APPLICANT: Suvanto, Petri
; APPLICANT: Trupp, Miles
; APPLICANT: Saarna, Mart
; TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor Receptors
; FILE REFERENCE: CEPH0418
; CURRENT APPLICATION NUMBER: US/10/673,007
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/08/861,990
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: 08/747,842
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: 60/006,619
; PRIOR FILING DATE: 1995-11-13
; PRIOR APPLICATION NUMBER: 60/015,767
; PRIOR FILING DATE: 1996-04-16
; PRIOR APPLICATION NUMBER: 60/021,965
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,638
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,639
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-673-007-8

Query Match 92.9%; Score 2310.5; DB 16; Length 465;

Best Local Similarity 92.5%; Pred. No. 3.1e-194;

Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

QY 1 MFATLTYFALPLDILMSAEVSGGRLDVCVKSDDCKECSCTKYRTLROCVAGKETNF 60
Db 1 MFATLTYFALPLDILMSAEVSGGRLDVCVKSDDCKECSCTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDEBCRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
Db 61 SLTSGLEAKDEBCRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
QY 121 YEPVNSRLSDTFRVVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
Db 121 YEPVNSRLSDTFRVVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCKHAKLROFPDVKVPAKHSYGMFLFCSCRDIACTERRRQTIIVPCSYEERER 240
Db 181 SVSNDVCCRCKHAKLROFPDVKVPAKHSYGMFLFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCNLSDSCSKTNYICRSLADFTFNCOPESRSVSNCLKENYADCLLAYSGLIGVTMTN 300
Db 241 PNCNLSDSCSKTNYICRSLADFTFNCOPESRSVSNCLKENYADCLLAYSGLIGVTMTN 300
QY 301 YVDSSSLVAPWCCDSNSGNDLEBCLKFNFKNTCLKNAIQAFGNSDVTVMQPAFPV 360
Db 301 YVDSSSLVAPWCCDSNSGNDLEBCLKFNFKNTCLKNAIQAFGNSDVTVMQPAFPV 360
QY 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSVSGSTHLCISDSDF 420
Db 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAOKLKSNSVSGSTHLCISDSDF 420

QY 421 GKDLGASSHTTKSMAAPSCSLSPVLM TALALSVLAETS 468
DB 421 EKEGL-GASSHTTKSMAAPSCSLSPVLM TALALSVLAETS 465

RESULT 11

US-10-155-693-6
Sequence 6, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOIAN
APPLICANT: MEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR FILING DATE: 1996-04-22
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 465
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (184)..(184)
OTHER INFORMATION: The 'Xaa' at location 184 stands for Lys, or Asn.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(510)
OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(539)
OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
FEATURE:
NAME/KEY: misc feature
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
FEATURE:
NAME/KEY: misc feature
LOCATION: (2256)..(2294)
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet
OTHER INFORMATION: ween different receptor clones
FEATURE:
NAME/KEY: misc feature
LOCATION: (1091)..(1091)
OTHER INFORMATION: N in position 1091 indicates any nucleic acid
US-10-155-693-6

Query Match 92.8%; Score 2309.5; DB 14; Length 465;

Best Local Similarity 92.5%; Pred. No. 3.7e-194;

Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

QY 1 MFLATYFALPLDLILMSAEVSGDRLDCVKASDQCKEOSTKRTTLRQCVAGKETNF 60
DB 1 MFLATYFALPLDLILMSAEVSGDRLDCVKASDQCKEOSTKRTTLRQCVAGKETNF 60
QY 61 SLTSGLEADDECSAWEALKQSLYNCRCRKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
DB 61 SLTSGLEADDECSAWEALKQSLYNCRCRKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
QY 121 YEFVNRSLSDIPRAVFIISDVFOVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180
DB 121 YEFVNRSLSDIPRAVFIISDVFOVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180

QY 181 SWSNEVNRKCKHAROFEDKVPAGSYGMLFCSCORDIACERRROTIVPVCSYERER 240
DB 181 SWSVDCNRRCKHAROFEDKVPAGSYGMLFCSCORDIACERRROTIVPVCSYERER 240
QY 241 PNCISLQDSCKTYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCISLQDSCKTYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YVDSLSVAPWPCDSCNSGNDLEDCIKFLNFKDNTCLNNAIQAFNGSDVTVMQPAFV 360
DB 301 YVDSLSVAPWPCDSCNSGNDLEDCIKFLNFKDNTCLNNAIQAFNGSDVTVMQPAFV 360
QY 361 QTTATTTTAFRKNRPLCPAGSENEIPHHVLPCCANLQAQKLSVSGTHCLSDSDF 420
DB 361 QTTATTTTAFRKNRPLCPAGSENEIPHHVLPCCANLQAQKLSVSGTHCLSDSDF 420
QY 421 GKDLGASSHTTKSMAAPSCSLSPVLM TALALSVLAETS 468
DB 421 EKEGL-GASSHTTKSMAAPSCSLSPVLM TALALSVLAETS 465

RESULT 12

US-10-155-693-10
Sequence 10, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOIAN
APPLICANT: MEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 463
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: The 'Xaa' at location 5 stands for Thr, Ala, Pro, or Ser.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(537)
OTHER INFORMATION: No. US20030175876A1e= "1 to 537 is -235 to 301 of Figure 5 21acon
NAME/KEY: misc feature
LOCATION: (550)..(550)
OTHER INFORMATION: N in position 550 indicates any nucleic acid
US-10-155-693-10

Query Match 92.7%; Score 2306.5; DB 14; Length 463;

Best Local Similarity 92.7%; Pred. No. 6.8e-194;

Matches 429; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 1 MFLATYFALPLDLILMSAEVSGDRLDCVKASDQCKEOSTKRTTLRQCVAGKETNF 60
DB 1 MFLATYFALPLDLILMSAEVSGDRLDCVKASDQCKEOSTKRTTLRQCVAGKETNF 60
QY 61 SLTSGLEADDECSAWEALKQSLYNCRCRKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
DB 61 SLTSGLEADDECSAWEALKQSLYNCRCRKGKKEKNCIRIYWSYQSLQGNLLEDSP 120
QY 121 YEFVNRSLSDIPRAVFIISDVFOVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180
DB 121 YEFVNRSLSDIPRAVFIISDVFOVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180

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Db      121 YEPVNSRLSDIFRVVFPISDVFOQVEHI:PKGNKCLDAKACNLDDICCKYRSAYITPCTT 180
QY      181 SMSNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVPKSYEBER 240
Db      181 SVSNDVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVPKSYEBER 240
QY      241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGVTMPN 300
Db      241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGVTMPN 300
QY      301 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 360
Db      301 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 360
QY      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLP:PCANLQAOQKLSNVSGTHTLCTSDSF 420
Db      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLP:PCANLQAOQKLSNVSGTHTLCTSDSF 420
QY      421 GKDGAGASHITTKSMAAPSCSLSPVLM:LTALALSLYS 463
Db      421 EKEGL-GASSHITTKSMAAPSCSLSPVLM:LTALALSLYS 462

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RESULT 13

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US-10-241-220-62
/ Sequence 62, Application US/10241220
/ Publication No. US20030146408A1
/ GENERAL INFORMATION:
/ APPLICANT: Frantz, Gretchen
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Phillips, Heidi
/ APPLICANT: Polakis, Paul
/ APPLICANT: Spencer, Susan
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wu, Thomas
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ FILE REFERENCE: P5010R1-US
/ CURRENT FILING DATE: 2002-12-13
/ CURRENT FILING DATE: 2002-12-13
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 62
/ LENGTH: 460
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-241-220-62

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Query Match      91.6%; Score 2278; DB 14; Length 460;
Best Local Similarity 91.7%; Pred. No. 2.2e-191;
Matches 429; Conservative 18; Mismatches 13; Indels 8; Gaps 3;

QY      1 MFLATLTFALVLLDLMSAEVSGGRDLDCVAKSDOCLKEQSCSTYKRTLRQCVAGKETNF 60
Db      1 MFLATLTFALVLLDLMSAEVSGGRDLDCVAKSDOCLKEQSCSTYKRTLRQCVAGKETNF 60
QY      61 SLTSGLEAKDCRSMEALKOKSLYNCRCKGMKEKNCRLTYMGMYSLOQNDLLEBP 120
Db      61 SLTSGLEAKDCRSMEALKOKSLYNCRCKGMKEKNCRLTYMGMYSLOQNDLLEBP 120
QY      121 YEPVNSRLSDIFRVVFPISDVFOQVEHI:SKGNKCLDAKACNLDDICCKYRSAYITPCTT 180
Db      121 YEPVNSRLSDIFRVVFPISDVFOQVEHI:SKGNKCLDAKACNLDDICCKYRSAYITPCTT 180
QY      181 SMSNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVPKSYEBER 240
Db      181 SMSNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVPKSYEBER 240
QY      241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGVTMPN 300
Db      241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGVTMPN 300
QY      301 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 360
Db      301 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 360

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Db      296 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 365
QY      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLP:PCANLQAOQKLSNVSGTHTLCTSDSF 420
Db      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLP:PCANLQAOQKLSNVSGTHTLCTSDSF 420
QY      421 GKDGAGASHITTKSMAAPSCSLSPVLM:LTALALSLYS 468
Db      421 EKEGL-GASSHITTKSMAAPSCSLSPVLM:LTALALSLYS 460

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RESULT 14

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US-10-155-693-16
/ Sequence 16, Application US/10155693
/ Publication No. US20030175876A1
/ GENERAL INFORMATION:
/ APPLICANT: FOX, GARY M.
/ APPLICANT: JING, SHUQIAN
/ APPLICANT: WEN, DUANZHI
/ TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
/ FILE REFERENCE: A-401C
/ CURRENT APPLICATION NUMBER: US/10/155,693
/ CURRENT FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US/08/837,199
/ PRIOR FILING DATE: 1997-04-14
/ PRIOR APPLICATION NUMBER: US 60/015,907
/ PRIOR FILING DATE: 1996-04-22
/ PRIOR APPLICATION NUMBER: US 60/017,221
/ PRIOR FILING DATE: 1996-05-09
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 294
/ TYPE: PRT
/ ORGANISM: HUMAN
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)-(2157)
/ OTHER INFORMATION: No. US20030175876A1e "1 to 2157 is 814 to 2971 of Figure 5 29b.c"
/ NAME/KEY: misc.feature
/ LOCATION: (1204)-(1242)
/ OTHER INFORMATION: N in positions 1204 to 1242 indicates positions of divergence bet
/ OTHER INFORMATION: ween different receptor clones.
US-10-155-693-16

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Query Match      57.5%; Score 1431.5; DB 14; Length 294;
Best Local Similarity 89.9%; Pred. No. 2.9e-117;
Matches 267; Conservative 17; Mismatches 10; Indels 3; Gaps 2;

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QY      172 SAYITPCTTSMNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVP 231
Db      1 SAYITPCTTSMNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVP 231
QY      232 VCSYEBERPNCLSHQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSG 291
Db      232 VCSYEBERPNCLSHQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSG 291
QY      61 VCSYEBERPNCLSHQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSG 120
Db      61 VCSYEBERPNCLSHQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSG 120
QY      121 YEPVNSRLSDIFRVVFPISDVFOQVEHI:SKGNKCLDAKACNLDDICCKYRSAYITPCTT 180
Db      121 YEPVNSRLSDIFRVVFPISDVFOQVEHI:SKGNKCLDAKACNLDDICCKYRSAYITPCTT 180
QY      181 SMSNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVPKSYEBER 240
Db      181 SMSNEVCNRKCKHAKLROFPDVKPAKSHYGM:FCSCRDIACTERRRQITVPKSYEBER 240
QY      241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGVTMPN 300
Db      241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCLKENYADCLAYSGLIGVTMPN 300
QY      301 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 360
Db      301 YVDSLSVAVAWCCSNGNDLEDCIKFLNFKONTCLKNAIQAFNGSDVTVMQAPAPV 360

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RESULT 15

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